

10/559097

AP16 Rec'd PCT/PTO 01 DEC 2005
SEQUENCE LISTING

<110> CropDesign N.V.

<120> Monocotyledonous plants having improved growth characteristics
and a method for making the same

<130> CD-097-PCT

<150> EP 03076719.8

<151> 2003-06-03

<160> 30

<170> PatentIn version 3.2

<210> 1

<211> 2313

<212> DNA

<213> Oryza sativa

<400> 1

gagaagagag	ttttgtagcg	agctcgcgcg	aatgcgaagc	caaccgagag	aggtctcgat	60
accaaatecc	gattttctca	cctgaatecc	ccccccacgt	tcctcgtttc	aatctgttcg	120
tctgcgaatc	gaattctttg	tttttttttc	tctaatttta	ccgggaattg	tcgaattagg	180
cattcaccaa	cgagcaagag	gggagtggat	tggttggtta	aagctccgca	tcttgccggc	240
gaaatctcgc	tctcttctct	gcggtgggtg	gccggagaag	tcgccgccgg	tgaggcatgg	300
ggatggaggt	ggcggcgggc	cggctggggg	ctctgtacac	gacctccgac	tacgcgtcgg	360
tggtgtccat	caacctgttc	gtcgcgctgc	tctgcgcctg	catcgtcctc	ggccacctcc	420
tcgaggagaa	tcgctgggtc	aatgagtcca	tcaccgcgct	catcatcggt	ctctgcaccg	480
gcgtggtgat	cttgctgatg	accaaaggga	agagctcgca	cttattcgtc	ttcagtggag	540
atctcttctt	catctacctc	ctccctccga	tcactctcaa	tgcaggtttt	caggtaaaga	600
aaaagcaatt	cttcgcgaat	ttcatgacga	tcacattatt	tggagccgtc	gggacaatga	660
tatccttttt	cacaatatct	attgctgccg	ttgcaatatt	cagcagaatg	aacattggaa	720
cgctggatgt	aggagatttt	cttgcaattg	gagccatctt	ttctgcgaca	gattctgtct	780
gcacattgca	ggctctcaat	caggatgaga	cacccttttt	gtacagtctg	gtattcgggt	840
aaggtgttgt	gaacgatgct	acatcaattg	tgcttttcaa	cgactacag	aactttgatc	900
ttgtccacat	agatgcggtc	gtcgttctga	aattcttggg	gaacttcttt	tatttatatt	960
tgctcgagcac	cttccttgga	gtatttgctg	gattgctcag	tgcatacata	atcaagaagc	1020
tatacattgg	aaggcattct	actgaccgtg	aggttgccct	tatgatgctc	atggcttacc	1080
tttcatatat	gctggctgag	ttgctagatt	tgagcggcat	tctcaccgta	ttcttctgtg	1140
gtattgtaat	gtcacattac	acttggcata	acgtcacaga	gagttcaaga	gttacaacaa	1200
agcacgcatt	tgcaactctg	tccttcattg	ctgagacttt	tctcttcctg	tatgttggga	1260
tgatgcatt	ggatattgaa	aaatgggagt	ttgccagtga	cagacctggc	aaatccattg	1320
ggataagctc	aattttgcta	ggattgggtc	tgattggaag	agctgctttt	gtattcccgc	1380
tgctgttctt	gtcgaacctc	acaaagaagg	caccgaatga	aaaaataacc	tgagacagc	1440
aagtgttaat	atggtgggct	gggctgatga	gaggagctgt	gtcgattgct	cttgcttaca	1500
ataagtttac	aagatctggc	catactcagc	tgacacggca	tgcaataatg	atcaccagca	1560
ccatcactgt	cgttcttttt	agcactatgg	tatttgggat	gatgacaaag	ccattgatca	1620
ggctgctgct	accggcctca	ggccatcctg	tcacctctga	gccttcatca	ccaaagtccc	1680
tgcatctctc	tctcctgaca	agcatgcaag	gttctgacct	cgagagtaca	accaacattg	1740
tgaggccttc	cagcctccgg	atgctcctca	ccaagccgac	ccacactgtc	cactactact	1800
ggcgcaagtt	cgacgacgcg	ctgatgcgac	cgatgttttg	cgggcgcggg	ttcgtgccct	1860
tctcccctgg	atcaccaacc	gagcagagcc	atggagggaag	atgaacagtg	caaagaaatg	1920
agaatggaat	ggttgatgag	gagaatacat	gtaaaatgtg	acagcaaaag	agagaaggca	1980
agttttgggt	ttgtagagtt	tggctgctgc	taatgagttg	ttgatagtgc	ctatattctt	2040
cagaacttca	gatggtgcct	caccaaggcc	taagagccag	gaggaccttc	tgataatggg	2100

tcgggatgat	tggtttgttc	tgtcaggatg	aaccctagtg	agtgacacag	ggtgatgtgc	2160
tccgacaacc	tgtaaatttt	gtagattaac	agccccattt	gtacctgtct	accatcttta	2220
gttggcgggt	gttctttcct	agttgccacc	ctgcatgtaa	aatgaaattc	tccgcacaaa	2280
tagatttggt	tgtataataa	ttttgcttgg	ttg			2313

<210> 2
 <211> 535
 <212> PRT
 <213> Oryza sativa

<400> 2

Met	Gly	Met	Glu	Val	Ala	Ala	Ala	Arg	Leu	Gly	Ala	Leu	Tyr	Thr	Thr	1	5	10	15
Ser	Asp	Tyr	Ala	Ser	Val	Val	Ser	Ile	Asn	Leu	Phe	Val	Ala	Leu	Leu	20	25	30	
Cys	Ala	Cys	Ile	Val	Leu	Gly	His	Leu	Leu	Glu	Glu	Asn	Arg	Trp	Val	35	40	45	
Asn	Glu	Ser	Ile	Thr	Ala	Leu	Ile	Ile	Gly	Leu	Cys	Thr	Gly	Val	Val	50	55	60	
Ile	Leu	Leu	Met	Thr	Lys	Gly	Lys	Ser	Ser	His	Leu	Phe	Val	Phe	Ser	65	70	75	80
Glu	Asp	Leu	Phe	Phe	Ile	Tyr	Leu	Leu	Pro	Pro	Ile	Ile	Phe	Asn	Ala	85	90	95	
Gly	Phe	Gln	Val	Lys	Lys	Lys	Gln	Phe	Phe	Arg	Asn	Phe	Met	Thr	Ile	100	105	110	
Thr	Leu	Phe	Gly	Ala	Val	Gly	Thr	Met	Ile	Ser	Phe	Phe	Thr	Ile	Ser	115	120	125	
Ile	Ala	Ala	Ile	Ala	Ile	Phe	Ser	Arg	Met	Asn	Ile	Gly	Thr	Leu	Asp	130	135	140	
Val	Gly	Asp	Phe	Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ser	Ala	Thr	Asp	Ser	145	150	155	160
Val	Cys	Thr	Leu	Gln	Val	Leu	Asn	Gln	Asp	Glu	Thr	Pro	Phe	Leu	Tyr	165	170	175	
Ser	Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Ile	Val	180	185	190	
Leu	Phe	Asn	Ala	Leu	Gln	Asn	Phe	Asp	Leu	Val	His	Ile	Asp	Ala	Ala	195	200	205	
Val	Val	Leu	Lys	Phe	Leu	Gly	Asn	Phe	Phe	Tyr	Leu	Phe	Leu	Ser	Ser	210	215	220	
Thr	Phe	Leu	Gly	Val	Phe	Ala	Gly	Leu	Leu	Ser	Ala	Tyr	Ile	Ile	Lys	225	230	235	240
Lys	Leu	Tyr	Ile	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala	Leu	Met				

245								250				255			
Met	Leu	Met	Ala	Tyr	Leu	Ser	Tyr	Met	Leu	Ala	Glu	Leu	Leu	Asp	Leu
			260						265				270		
Ser	Gly	Ile	Leu	Thr	Val	Phe	Phe	Cys	Gly	Ile	Val	Met	Ser	His	Tyr
		275					280					285			
Thr	Trp	His	Asn	Val	Thr	Glu	Ser	Ser	Arg	Val	Thr	Thr	Lys	His	Ala
	290					295					300				
Phe	Ala	Thr	Leu	Ser	Phe	Ile	Ala	Glu	Thr	Phe	Leu	Phe	Leu	Tyr	Val
305					310					315					320
Gly	Met	Asp	Ala	Leu	Asp	Ile	Glu	Lys	Trp	Glu	Phe	Ala	Ser	Asp	Arg
			325						330					335	
Pro	Gly	Lys	Ser	Ile	Gly	Ile	Ser	Ser	Ile	Leu	Leu	Gly	Leu	Val	Leu
			340						345				350		
Ile	Gly	Arg	Ala	Ala	Phe	Val	Phe	Pro	Leu	Ser	Phe	Leu	Ser	Asn	Leu
		355					360					365			
Thr	Lys	Lys	Ala	Pro	Asn	Glu	Lys	Ile	Thr	Trp	Arg	Gln	Gln	Val	Val
	370					375					380				
Ile	Trp	Trp	Ala	Gly	Leu	Met	Arg	Gly	Ala	Val	Ser	Ile	Ala	Leu	Ala
385					390					395					400
Tyr	Asn	Lys	Phe	Thr	Arg	Ser	Gly	His	Thr	Gln	Leu	His	Gly	Asn	Ala
			405						410					415	
Ile	Met	Ile	Thr	Ser	Thr	Ile	Thr	Val	Val	Leu	Phe	Ser	Thr	Met	Val
			420						425				430		
Phe	Gly	Met	Met	Thr	Lys	Pro	Leu	Ile	Arg	Leu	Leu	Leu	Pro	Ala	Ser
		435					440					445			
Gly	His	Pro	Val	Thr	Ser	Glu	Pro	Ser	Ser	Pro	Lys	Ser	Leu	His	Ser
	450					455					460				
Pro	Leu	Leu	Thr	Ser	Met	Gln	Gly	Ser	Asp	Leu	Glu	Ser	Thr	Thr	Asn
465					470					475					480
Ile	Val	Arg	Pro	Ser	Ser	Leu	Arg	Met	Leu	Leu	Thr	Lys	Pro	Thr	His
			485						490					495	
Thr	Val	His	Tyr	Tyr	Trp	Arg	Lys	Phe	Asp	Asp	Ala	Leu	Met	Arg	Pro
			500						505				510		
Met	Phe	Gly	Gly	Arg	Gly	Phe	Val	Pro	Phe	Ser	Pro	Gly	Ser	Pro	Thr
		515					520					525			
Glu	Gln	Ser	His	Gly	Gly	Arg									
	530					535									

<211> 1614
 <212> DNA
 <213> Arabidopsis thaliana

<400> 3
 atgttggatt ctctagtgtc gaaactgcct tcgttatcga catctgatca cgcttctgtg 60
 gttgcgttga atctctttgt tgcacttctt tgtgcttgta ttgttcttgg tcatcttttg 120
 gaagagaata gatggatgaa cgaatccatc accgccttgt tgattgggct aggcactggg 180
 gttaccattt tgttgattag taaaggaaaa agctcgcatac ttctcgtctt tagtgaagat 240
 cttttcttca tatatctttt gccacccatt atattcaatg cagggtttca agtaaaaaag 300
 aagcagtttt tccgcaattt cgtgactatt atgctttttg gtgctgttgg gactattatt 360
 tcttgacaaa tcatatctct aggtgtaaca cagttcttta agaagttgga cattggaacc 420
 tttgacttgg gtgattatct tgctatttgg gccatatttg ctgcaacaga ttcagtatgt 480
 aactgcagg ttctgaatca agacgagaca cctttgcttt acagtcttgt attcggagag 540
 ggtgttgtga atgatgcaac gtcagttgtg gtcttcaacg cgattcagag ctttgatctc 600
 actcacctaa accacgaagc tgcttttcat cttcttggaa acttcttga tttgtttctc 660
 ctaagtacct tgcttgggtc tgcaaccggt ctgataagtg cgtatgttat caagaagcta 720
 tactttggaa ggcactcaac tgaccgagag gttgccctta tgatgcttat ggcgtatctt 780
 tcttataatgc ttgctgagct tttcgacttg agcggtatcc tcaactgtgtt tttctgtggt 840
 attgtgatgt cccattacac atggcacaaat gtaacggaga gctcaagaat aacaacaaaag 900
 catacctttg caactttgtc atttcttgcg gagacattta ttttcttgta tgttggaaatg 960
 gatgccttgg acattgacaa gtggagatcc gtgagtgaaca caccgggaac atcgatcgca 1020
 gtgagctcaa tcctaatggg tctggatcatg gttggaagag cagcgttcgt ctttccgtta 1080
 tcgtttctat ctaacttagc caagaagaat caaagcgaga aaatcaactt taacatgcag 1140
 gttgtgattt ggtggtctgg tctcatgaga ggtgctgtat ctatggctct tgcatacaac 1200
 aagtttacaa gggccgggca cacagatgta cgcgggaatg caatcatgat cagcagtagc 1260
 ataactgtct gtcttttttag cacagtgggtg tttggtatgc tgaccaaacc actcataagc 1320
 tacctattac cgcaccagaa cgccaccacg agcatgttat ctgatgacaa caccacaaa 1380
 tccatacata tccctttgtt ggaccaagac tcgttcattg agccttcagg gaaccacaat 1440
 gtgcctcggc ctgacagtat acgtggcttc ttgacacggc ccaactcgaac cgtgcattac 1500
 tactggagac aatttgatga ctcttcatg cgaccctgtc ttggaggctg tggctttgta 1560
 ccctttgttc caggttctcc aactgagaga aacctcctg atcttagtaa ggct 1614

<210> 4
 <211> 538
 <212> PRT
 <213> Arabidopsis thaliana

<400> 4
 Met Leu Asp Ser Leu Val Ser Lys Leu Pro Ser Leu Ser Thr Ser Asp
 1 5 10 15
 His Ala Ser Val Val Ala Leu Asn Leu Phe Val Ala Leu Leu Cys Ala
 20 25 30
 Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu
 35 40 45
 Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
 50 55 60
 Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
 65 70 75 80
 Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
 85 90 95

Gln	Val	Lys	Lys	Lys	Gln	Phe	Phe	Arg	Asn	Phe	Val	Thr	Ile	Met	Leu	
		100						105					110			
Phe	Gly	Ala	Val	Gly	Thr	Ile	Ile	Ser	Cys	Thr	Ile	Ile	Ser	Leu	Gly	
		115					120					125				
Val	Thr	Gln	Phe	Phe	Lys	Lys	Leu	Asp	Ile	Gly	Thr	Phe	Asp	Leu	Gly	
	130					135					140					
Asp	Tyr	Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ala	Ala	Thr	Asp	Ser	Val	Cys	
145					150					155					160	
Thr	Leu	Gln	Val	Leu	Asn	Gln	Asp	Glu	Thr	Pro	Leu	Leu	Tyr	Ser	Leu	
			165						170					175		
Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Val	Val	Val	Phe	
			180					185					190			
Asn	Ala	Ile	Gln	Ser	Phe	Asp	Leu	Thr	His	Leu	Asn	His	Glu	Ala	Ala	
		195					200					205				
Phe	His	Leu	Leu	Gly	Asn	Phe	Leu	Tyr	Leu	Phe	Leu	Leu	Ser	Thr	Leu	
	210					215					220					
Leu	Gly	Ala	Ala	Thr	Gly	Leu	Ile	Ser	Ala	Tyr	Val	Ile	Lys	Lys	Leu	
225					230					235					240	
Tyr	Phe	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala	Leu	Met	Met	Leu	
			245						250					255		
Met	Ala	Tyr	Leu	Ser	Tyr	Met	Leu	Ala	Glu	Leu	Phe	Asp	Leu	Ser	Gly	
		260						265					270			
Ile	Leu	Thr	Val	Phe	Phe	Cys	Gly	Ile	Val	Met	Ser	His	Tyr	Thr	Trp	
		275					280					285				
His	Asn	Val	Thr	Glu	Ser	Ser	Arg	Ile	Thr	Thr	Lys	His	Thr	Phe	Ala	
	290					295					300					
Thr	Leu	Ser	Phe	Leu	Ala	Glu	Thr	Phe	Ile	Phe	Leu	Tyr	Val	Gly	Met	
305					310					315					320	
Asp	Ala	Leu	Asp	Ile	Asp	Lys	Trp	Arg	Ser	Val	Ser	Asp	Thr	Pro	Gly	
			325						330					335		
Thr	Ser	Ile	Ala	Val	Ser	Ser	Ile	Leu	Met	Gly	Leu	Val	Met	Val	Gly	
		340						345					350			
Arg	Ala	Ala	Phe	Val	Phe	Pro	Leu	Ser	Phe	Leu	Ser	Asn	Leu	Ala	Lys	
		355					360					365				
Lys	Asn	Gln	Ser	Glu	Lys	Ile	Asn	Phe	Asn	Met	Gln	Val	Val	Ile	Trp	
	370					375					380					
Trp	Ser	Gly	Leu	Met	Arg	Gly	Ala	Val	Ser	Met	Ala	Leu	Ala	Tyr	Asn	
385					390					395					400	

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met
405 410 415

tgactaaaaa	atcacaacat	cagaagat	ttt	ccttcagaca	gcaagttatc	atttggtggg	1500
ctgggtcttat	gagaggtgct	gtttcaatgg	cacttgcgta	taatcagttc	accatgtcgg		1560
ggcataactca	actacgtagc	aatgcaatca	tgataaccag	caccatcact	gttgtccttt		1620
tcagcacagt	ggtgtttggt	ttgctgacta	agccactcat	aaggcttcta	ctacctcatc		1680
ctaaaatcac	aagcagcatg	acaaccacag	aatcgactac	tccaaaatca	ttcattgtcc		1740
cacttctagg	agattcccga	gattctgaag	ctgatcttga	aggccatgaa	attcaccgac		1800
cgaacagcct	tcgtgcttta	ctatcaactc	caactcacac	tgttcatcga	ttatggcgaa		1860
agtttgatga	ttcattcatg	cgtcctgttt	ttggtggcag	aggttttgtt	cctgtagaac		1920
ctggctcacc	aagtgaacgc	aatggtaatc	aatgggggtg	agaaaagaag	ccatgaaatg		1980
tgtaatatgt	gttgatatac	acgtatgatt	tgtgaaaagt	catgcaacgt	gtgtataatg		2040
tatttattgc	ataagaacct	agtagtgaaa	tttttcttta	aaaaaaaaacc	tcgtagtga		2100
attttgttga	gctgtttgag	tagctagtat	gagatggcct	gccatctctc	tgtctattat		2160
gtaaaactaca	atatttttta	gattctctga	gccattacat	gtttgtgtat	gtgtccaaaa		2220
aaaaaaaaaa	aa						2232

<210> 6
 <211> 541
 <212> PRT
 <213> Medicago sativa

<400> 6

Met	Ala	Ile	Glu	Met	Ser	Ser	Ile	Val	Ser	Lys	Leu	Ser	Met	Leu	Ser
1				5					10					15	
Thr	Ser	Asp	His	Ala	Ser	Val	Val	Ser	Met	Asn	Leu	Phe	Val	Ala	Leu
			20					25					30		
Leu	Cys	Ala	Cys	Ile	Val	Leu	Gly	His	Leu	Leu	Glu	Glu	Asn	Arg	Trp
		35					40					45			
Met	Asn	Glu	Ser	Ile	Thr	Ala	Leu	Leu	Ile	Gly	Ile	Cys	Thr	Gly	Val
	50					55					60				
Val	Ile	Leu	Leu	Phe	Ser	Gly	Gly	Lys	Ser	Ser	His	Ile	Leu	Val	Phe
65					70				75						80
Ser	Glu	Asp	Leu	Phe	Phe	Ile	Tyr	Leu	Leu	Pro	Pro	Ile	Ile	Phe	Asn
				85					90					95	
Ala	Gly	Phe	Gln	Val	Lys	Lys	Lys	Gln	Phe	Phe	Val	Asn	Phe	Met	Thr
			100					105					110		
Ile	Thr	Ser	Phe	Gly	Ala	Ile	Gly	Thr	Leu	Ile	Ser	Cys	Val	Ile	Ile
		115					120					125			
Thr	Thr	Gly	Ala	Thr	Phe	Ala	Phe	Lys	Arg	Met	Asp	Ile	Gly	Pro	Leu
	130					135					140				
Glu	Ile	Gly	Asp	Tyr	Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ala	Ala	Thr	Asp
145					150				155						160
Ser	Val	Cys	Thr	Leu	Gln	Val	Leu	Asn	Gln	Asp	Glu	Thr	Pro	Leu	Leu
				165					170					175	
Tyr	Ser	Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Val
			180					185					190		

Val	Leu	Phe	Asn	Ala	Ile	Gln	Ser	Phe	Asp	Leu	Asn	Gln	Leu	Asn	Pro	195	200	205
Ser	Ile	Ala	Leu	His	Phe	Leu	Gly	Asn	Phe	Leu	Tyr	Leu	Phe	Val	Ala	210	215	220
Ser	Thr	Leu	Leu	Gly	Val	Val	Thr	Gly	Leu	Leu	Ser	Ala	Tyr	Val	Ile	225	230	235
Lys	Lys	Leu	Tyr	Ile	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala	Leu	245	250	255
Met	Met	Leu	Met	Ala	Tyr	Leu	Ser	Tyr	Met	Leu	Ala	Glu	Leu	Thr	Tyr	260	265	270
Leu	Ser	Gly	Ile	Leu	Thr	Val	Phe	Phe	Cys	Gly	Ile	Val	Met	Ser	His	275	280	285
Tyr	Thr	Trp	His	Asn	Val	Thr	Gln	Ser	Ser	Arg	Ile	Thr	Thr	Lys	His	290	295	300
Ser	Phe	Ala	Thr	Leu	Ser	Phe	Val	Ala	Glu	Ile	Phe	Ile	Phe	Leu	Tyr	305	310	315
Val	Gly	Met	Asp	Ala	Leu	Asp	Ile	Glu	Lys	Trp	Lys	Phe	Val	Ser	Asp	325	330	335
Ser	Pro	Gly	Thr	Ser	Ile	Ala	Ala	Ser	Ser	Val	Leu	Leu	Gly	Leu	Ile	340	345	350
Leu	Leu	Gly	Arg	Ala	Ala	Phe	Val	Phe	Pro	Leu	Ser	Phe	Leu	Ser	Asn	355	360	365
Leu	Thr	Lys	Lys	Ser	Gln	His	Gln	Lys	Ile	Ser	Phe	Arg	Gln	Gln	Val	370	375	380
Ile	Ile	Trp	Trp	Ala	Gly	Leu	Met	Arg	Gly	Ala	Val	Ser	Met	Ala	Leu	385	390	395
Ala	Tyr	Asn	Gln	Phe	Thr	Met	Ser	Gly	His	Thr	Gln	Leu	Arg	Ser	Asn	405	410	415
Ala	Ile	Met	Ile	Thr	Ser	Thr	Ile	Thr	Val	Val	Leu	Phe	Ser	Thr	Val	420	425	430
Val	Phe	Gly	Leu	Leu	Thr	Lys	Pro	Leu	Ile	Arg	Leu	Leu	Leu	Pro	His	435	440	445
Pro	Lys	Ile	Thr	Ser	Ser	Met	Thr	Thr	Thr	Glu	Ser	Thr	Thr	Pro	Lys	450	455	460
Ser	Phe	Ile	Val	Pro	Leu	Leu	Gly	Asp	Ser	Arg	Asp	Ser	Glu	Ala	Asp	465	470	475
Leu	Glu	Gly	His	Glu	Ile	His	Arg	Pro	Asn	Ser	Leu	Arg	Ala	Leu	Leu	485	490	495

Ser Thr Pro Thr His Thr Val His Arg Leu Trp Arg Lys Phe Asp Asp
500 505 510

Ser Phe Met Arg Pro Val Phe Gly Gly Arg Gly Phe Val Pro Val Glu
515 520 525

Pro Gly Ser Pro Ser Glu Arg Asn Gly Asn Gln Trp Gly
530 535 540

<210> 7
<211> 2263
<212> DNA
<213> Suaeda maritima subsp. salsa

<400> 7
tttcacaaag attattggac ttcagaagtt tgattttgtg gagctagaaa gggtttcaca 60
tacattggac attaatttac ttgaatatat atatatttgt tgtgggtcct ggattcgggt 120
gcacaaagaa ataggtgaac aatgttgta cagttgagct ctttttttgc aagtaagatg 180
gacatggttt cgacgtctga tcatgcttcc gttgtttcga tgaatttgtt tgtggcactg 240
ttacgtggct gcattgtaat tggatcatct ctcgaagaga atcgctggat gaatgaatcc 300
attacagctt tgctaataagg tttatctact gggattataa tcctgctaatt tagtggagga 360
aagagttcgc atttgttggc cttcagtgaa gatcttttct ttatatacct ccttccaccg 420
attatattca atgcgggggt tcaggtgaaa aagaagcaat ttttccgcaa cttcattact 480
attattttgt ttggagccgt tggatcattg gtatcattca taatcatac tcttggttca 540
atagctatat ttcaaaaagat ggatatttgt tgcgtggagt taggggatct tcttgcaatt 600
ggtgcaatat tcgctgcaac tgattcagtt tgcacattgc aagtgcctaa tcaagatgag 660
actccacttc tttatagtct cgtgttttgt gaaggtgtcg tcaatgatgc tacatcagtg 720
gtgttgttca atgcaattca aaactttgac ctcacgcaca ttgaccacag aattgccttc 780
caatttgggt gcaactttct atattttatt tttgcaagca ctctgcttgg agcagtgact 840
ggcttgctaa gcgcttatgt catcaaaaag ttgtactttg gaaggcattc aactgaccgt 900
gaggtagcct taatgatgct tatggcttat ctatcgtaca tgcttgctga actcttctat 960
ctgagcggaa ttcttacagt attcttctgt gggattgtca tgtcccataa tacatggcac 1020
aatgtgacgg agagctccag agtaaccacc aagcatgctt ttgcaacact ctcttttgta 1080
gctgagatct tcatctttct atatgttggg atggatgcac tggatattga gaagtggaga 1140
tttgtgagcg atagtcttg aacatctgtt gctgtgagtt ccatactgct tggctctcac 1200
atggttgggc gagctgcttt tgtttttccc ttgcctttt taatgaactt gtccaagaaa 1260
tcaaatagtg agaaggtcac cttcaatcag cagatagtca tttggtgggc tggctctcatg 1320
aaaagtgtcg tctccgtggc acttgcttat aatcagtttt caaggtcagg acacacacag 1380
ctgaggggaa atgcaatcat gattacaagc accataaccg ttgtcctttt cagtacgatg 1440
gtatttgggt tgctgacaaa gcctcttata ctctttatgt tgctcaacc gaaacatttc 1500
actagtcaa gcaccgtgtc agatttgggg agtccaaagt cattctcctt gcctcttctt 1560
gaagatagac aagattctga agctgatttg ggcaacgatg atgaagaagc ctacccccgt 1620
gggactatag ctgcacctac tagtcttctg atgctactaa atgcaccaac tcacactgtc 1680
catcattatt ggcgcagatt cgatgattat ttcatgcggc ctgtatttgg tggccggggg 1740
tttgtacctt ttgtcccagg ttcacccacc gaacagagca tcactaattt tgtcacagag 1800
aacataagtt agcgataatt gaggcagttg gtgcagaac taataactta cagccctaca 1860
ggcaatctac aaagacaaaa aatgccctta cccaagaacg aacagcccgg tgtttggtct 1920
cgtgggcttg atgttaagac tgtgctgtac ttctgttaat agagagtaag ttacagaaac 1980
caccgattha aacatatctg taatttttta cagcatggat attcgatgca ttctttaatc 2040
tggctgtagc tagaatactc tagcatgttt tgtagtttca gtcttaccat ttaggttttc 2100
tcctacataa cctcaataag ctgttttagt tgcttactgc ttactttaga gcaaaactgca 2160
actgtgaaaa ttgcttacgt cagcggcacc tgtgtaattt atcattttta taatgatgga 2220
gcatgatcat ttgcaatcaa atttacaata ctgtgattaa aaa 2263

<210> 8
<211> 556
<212> PRT

<213> Suaeda maritima subsp. salsa

<400> 8

Met	Leu	Ser	Gln	Leu	Ser	Ser	Phe	Phe	Ala	Ser	Lys	Met	Asp	Met	Val
1			5						10					15	
Ser	Thr	Ser	Asp	His	Ala	Ser	Val	Val	Ser	Met	Asn	Leu	Phe	Val	Ala
			20					25					30		
Leu	Leu	Arg	Gly	Cys	Ile	Val	Ile	Gly	His	Leu	Leu	Glu	Glu	Asn	Arg
		35					40					45			
Trp	Met	Asn	Glu	Ser	Ile	Thr	Ala	Leu	Leu	Ile	Gly	Leu	Ser	Thr	Gly
	50					55					60				
Ile	Ile	Ile	Leu	Leu	Ile	Ser	Gly	Gly	Lys	Ser	Ser	His	Leu	Leu	Val
65					70				75						80
Phe	Ser	Glu	Asp	Leu	Phe	Phe	Ile	Tyr	Leu	Leu	Pro	Pro	Ile	Ile	Phe
			85						90					95	
Asn	Ala	Gly	Phe	Gln	Val	Lys	Lys	Lys	Gln	Phe	Phe	Arg	Asn	Phe	Ile
		100						105					110		
Thr	Ile	Ile	Leu	Phe	Gly	Ala	Val	Gly	Thr	Leu	Val	Ser	Phe	Ile	Ile
		115					120					125			
Ile	Ser	Leu	Gly	Ser	Ile	Ala	Ile	Phe	Gln	Lys	Met	Asp	Ile	Gly	Ser
	130					135					140				
Leu	Glu	Leu	Gly	Asp	Leu	Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ala	Ala	Thr
145					150				155						160
Asp	Ser	Val	Cys	Thr	Leu	Gln	Val	Leu	Asn	Gln	Asp	Glu	Thr	Pro	Leu
			165						170					175	
Leu	Tyr	Ser	Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser
			180					185					190		
Val	Val	Leu	Phe	Asn	Ala	Ile	Gln	Asn	Phe	Asp	Leu	Thr	His	Ile	Asp
		195					200					205			
His	Arg	Ile	Ala	Phe	Gln	Phe	Gly	Gly	Asn	Phe	Leu	Tyr	Leu	Phe	Phe
	210					215					220				
Ala	Ser	Thr	Leu	Leu	Gly	Ala	Val	Thr	Gly	Leu	Leu	Ser	Ala	Tyr	Val
225					230					235					240
Ile	Lys	Lys	Leu	Tyr	Phe	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala
			245						250					255	
Leu	Met	Met	Leu	Met	Ala	Tyr	Leu	Ser	Tyr	Met	Leu	Ala	Glu	Leu	Phe
			260					265					270		
Tyr	Leu	Ser	Gly	Ile	Leu	Thr	Val	Phe	Phe	Cys	Gly	Ile	Val	Met	Ser
		275					280					285			

His Tyr Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys
290 295 300

His Ala Phe Ala Thr Leu Ser Phe Val Ala Glu Ile Phe Ile Phe Leu
305 310 315 320

Tyr Val Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Arg Phe Val Ser
325 330 335

Asp Ser Pro Gly Thr Ser Val Ala Val Ser Ser Ile Leu Leu Gly Leu
340 345 350

His Met Val Gly Arg Ala Ala Phe Val Phe Pro Phe Ala Phe Leu Met
355 360 365

Asn Leu Ser Lys Lys Ser Asn Ser Glu Lys Val Thr Phe Asn Gln Gln
370 375 380

Ile Val Ile Trp Trp Ala Gly Leu Met Lys Ser Ala Val Ser Val Ala
385 390 395 400

Leu Ala Tyr Asn Gln Phe Ser Arg Ser Gly His Thr Gln Leu Arg Gly
405 410 415

Asn Ala Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr
420 425 430

Met Val Phe Gly Leu Leu Thr Lys Pro Leu Ile Leu Phe Met Leu Pro
435 440 445

Gln Pro Lys His Phe Thr Ser Ala Ser Thr Val Ser Asp Leu Gly Ser
450 455 460

Pro Lys Ser Phe Ser Leu Pro Leu Leu Glu Asp Arg Gln Asp Ser Glu
465 470 475 480

Ala Asp Leu Gly Asn Asp Asp Glu Glu Ala Tyr Pro Arg Gly Thr Ile
485 490 495

Ala Arg Pro Thr Ser Leu Arg Met Leu Leu Asn Ala Pro Thr His Thr
500 505 510

Val His His Tyr Trp Arg Arg Phe Asp Asp Tyr Phe Met Arg Pro Val
515 520 525

Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr Glu
530 535 540

Gln Ser Ile Thr Asn Phe Val Thr Glu Asn Ile Ser
545 550 555

<210> 9
<211> 1623
<212> DNA
<213> Zea mays

<400> 9

atggggccttg	gagtagtggc	ggagctagtc	cgccttggcg	tcctttcctc	cacctcagat	60
cacgcctccg	tggtttagcat	caatctcttt	gtcgccttgc	tctgcgcctg	tatcgtcctg	120
ggccatcttc	ttgaagagaa	taggtgggtg	aacgagtcca	ccgcgctgat	tgtcgggctc	180
ggcaccggta	ccgtcatcct	catgattagc	cgggggggtg	ttattcacgt	cctagtcttc	240
tccgaggacc	tcttcttctt	ctatcttttg	ccgccgatca	ttttcaatgc	agggttccaa	300
gtgaagaaga	aacagttctt	tcgaaacttc	attactatta	cactgtttgg	tgcaattggc	360
accttgatct	cttttactgt	aatatccctt	ggcgtcttag	gactaatatc	aaggcttaat	420
atcggcgcac	ttgaactggg	agactatctt	gcacttgggg	caatattctc	ggccacagac	480
tccggttgca	ccttgccagg	gttaagccaa	gatgagacac	cattcttgta	cagtcttgta	540
ttcgggtgaag	gcgtgggtcaa	cgatgccact	tccgtagtgg	tggtcaatgc	actccaaaac	600
tttgatataa	ctcacatcga	tgcggagggt	gtcttccatc	tattaggaaa	cttcttctac	660
ctcttccttc	tatcaactgt	gttgggagtg	gccacaggac	ttatctcagc	gttagtgatt	720
aaaaagctat	actttggacg	gcactctact	gacaggggag	tggtctttat	gatgcttatg	780
gcgtatctct	cctacatgtt	ggcggaaact	ttcgcgctga	gcgggatctt	gacgggtatt	840
tttgggtgca	ttgttatgag	ccactataca	tggcacaacg	tgacagagtc	cagcagaatc	900
acgactaagc	atgcgtttgc	cacgctcagc	ttcctagccg	aaaccttcct	ctttctgtac	960
gtgggtatgg	atgctctcga	cattgacaag	tggaggtccg	tgagtgcac	cccaggtaag	1020
tctctggcca	taagctcgat	tttgatggga	ctcgtgatgg	ttggccgggc	tgcttctgta	1080
ttccctctct	ccttcctctc	caatttagcg	aaaaaaacgg	agcacgaaaa	aatcagctgg	1140
aagcagcagg	tggtcatttg	gtgggcgggt	ctcatgcgag	gcgccgtttc	gatggcccta	1200
gcgtacaaga	agtttaccgg	cgcaggggcat	actcaggtcc	gcgggaacgc	gatcatgatt	1260
accagcacga	ttatcgctcg	gttgttttcg	acaatgggtg	tcggcctgct	cacgaagccc	1320
ttaattaact	tgctaatacc	gcaccgtaac	gccacatcga	tgttgagcga	tgactcaagc	1380
ccaaagtcct	tgcatagccc	tctgctaacc	tctcaactcg	gtagcgactt	agaggagccg	1440
accaacatcc	cgcgcccgag	ctccataaga	ggcgagttcc	tcaccatgac	taggaccgtg	1500
caccgatact	ggcgcaagtt	cgacgacgcc	ttcatgaggc	ccatgttcgg	aggccgcggg	1560
ttcgtacctt	tcgtgccagg	cagcccagacc	gagcgtaatc	cgccggatct	ttccaaggct	1620
taa						1623

<210> 10
 <211> 540
 <212> PRT
 <213> Zea mays

<400> 10
 Met Gly Leu Gly Val Val Ala Glu Leu Val Arg Leu Gly Val Leu Ser
 1 5 10 15

Ser Thr Ser Asp His Ala Ser Val Val Ser Ile Asn Leu Phe Val Ala
 20 25 30

Leu Leu Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg
 35 40 45

Trp Val Asn Glu Ser Thr Ala Leu Ile Val Gly Leu Gly Thr Gly Thr
 50 55 60

Val Ile Leu Met Ile Ser Arg Gly Val Val Ile His Val Leu Val Phe
 65 70 75 80

Ser Glu Asp Leu Phe Phe Phe Tyr Leu Leu Pro Pro Ile Ile Phe Asn
 85 90 95

Ala Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Ile Thr
 100 105 110

Ile Thr Leu Phe Gly Ala Val Gly Thr Leu Ile Ser Phe Thr Val Ile

115					120					125					
Ser	Leu	Gly	Ala	Leu	Gly	Leu	Ile	Ser	Arg	Leu	Asn	Ile	Gly	Ala	Leu
130						135					140				
Glu	Leu	Gly	Asp	Tyr	Leu	Ala	Leu	Gly	Ala	Ile	Phe	Ser	Ala	Thr	Asp
145					150					155					160
Ser	Val	Cys	Thr	Leu	Gln	Val	Leu	Ser	Gln	Asp	Glu	Thr	Pro	Phe	Leu
				165					170					175	
Tyr	Ser	Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Val
			180					185					190		
Val	Val	Phe	Asn	Ala	Leu	Gln	Asn	Phe	Asp	Ile	Thr	His	Ile	Asp	Ala
		195					200					205			
Glu	Val	Val	Phe	His	Leu	Leu	Gly	Asn	Phe	Phe	Tyr	Leu	Phe	Leu	Leu
210						215					220				
Ser	Thr	Val	Leu	Gly	Val	Ala	Thr	Gly	Leu	Ile	Ser	Ala	Leu	Val	Ile
225					230					235					240
Lys	Lys	Leu	Tyr	Phe	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala	Leu
				245					250					255	
Met	Met	Leu	Met	Ala	Tyr	Leu	Ser	Tyr	Met	Leu	Ala	Glu	Leu	Phe	Ala
			260					265					270		
Leu	Ser	Gly	Ile	Leu	Thr	Val	Phe	Phe	Gly	Cys	Ile	Val	Met	Ser	His
		275					280					285			
Tyr	Thr	Trp	His	Asn	Val	Thr	Glu	Ser	Ser	Arg	Ile	Thr	Thr	Lys	His
		290					295				300				
Ala	Phe	Ala	Thr	Leu	Ser	Phe	Leu	Ala	Glu	Thr	Phe	Leu	Phe	Leu	Tyr
305					310					315					320
Val	Gly	Met	Asp	Ala	Leu	Asp	Ile	Asp	Lys	Trp	Arg	Ser	Val	Ser	Asp
				325					330					335	
Thr	Pro	Gly	Lys	Ser	Leu	Ala	Ile	Ser	Ser	Ile	Leu	Met	Gly	Leu	Val
			340					345					350		
Met	Val	Gly	Arg	Ala	Ala	Phe	Val	Phe	Pro	Leu	Ser	Phe	Leu	Ser	Asn
		355					360					365			
Leu	Ala	Lys	Lys	Thr	Glu	His	Glu	Lys	Ile	Ser	Trp	Lys	Gln	Gln	Val
370						375					380				
Val	Ile	Trp	Trp	Ala	Gly	Leu	Met	Arg	Gly	Ala	Val	Ser	Met	Ala	Leu
385					390					395					400
Ala	Tyr	Lys	Lys	Phe	Thr	Arg	Ala	Gly	His	Thr	Gln	Val	Arg	Gly	Asn
				405					410					415	
Ala	Ile	Met	Ile	Thr	Ser	Thr	Ile	Ile	Val	Val	Leu	Phe	Ser	Thr	Met

420

425

430

Val Phe Gly Leu Leu Thr Lys Pro Leu Ile Asn Leu Leu Ile Pro His
435 440 445

Arg Asn Ala Thr Ser Met Leu Ser Asp Asp Ser Ser Pro Lys Ser Leu
450 455 460

His Ser Pro Leu Leu Thr Ser Gln Leu Gly Ser Asp Leu Glu Glu Pro
465 470 475 480

Thr Asn Ile Pro Arg Pro Ser Ser Ile Arg Gly Glu Phe Leu Thr Met
485 490 495

Thr Arg Thr Val His Arg Tyr Trp Arg Lys Phe Asp Asp Ala Phe Met
500 505 510

Arg Pro Met Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser
515 520 525

Pro Thr Glu Arg Asn Pro Pro Asp Leu Ser Lys Ala
530 535 540

<210> 11
<211> 1623
<212> DNA
<213> Zea mays

<400> 11
atgggccttg gtgttgatgc ggagacggtc aggcctcggag tccttagctc gacctcggat 60
catgccagcg ttgtcagtaa caacttcttc gtagcacttc tttgcgcctg tatcgtcctc 120
gggcatctct tggaggagaa ccgaatgggtt aatgagtcta ttacagcact gctgggtggg 180
ctgggcactg ggaccgtgat tctgatgatt agtcggggcg tgagtattca cgttctcgtc 240
ttttcagagg acctgttctt tatctatctg ttacctccga ttatcttcaa tgccgggttt 300
caagtaaaga aaaagcaatt cttccgcaac tttataacga ttattttgtt tgggtgctatt 360
gggactctga tttcctttgt aataatctct cttggtgcta tggggttgtt caagaaactt 420
gatgttggtc cactcgagct tggggactat cttgcaattg gtgctatttt ctcggcaaca 480
gattctgttt gcaccttaca ggtgcttaac caggatgaaa caccctact ctacagtctc 540
gtattcggcg agggcggttg taatgatgct acctcaatcg ttgtgttcaa cgcgctccaa 600
aacttcgaca tcacccacat caatgccgag gtgggtatttc acctccttgg caacttcttg 660
tacctcttcc tattgagcac cgtgctcggc gtggcgaccg gtctcatctc cgcgctggtc 720
attaagaaga tctacttcgg acgccactcg actgatcggg aagtggcctt aatgatgctg 780
atggcatatc taagctacat gctggcagag ctttttgccc tgtccggaat cctcactgtg 840
tttttcggct gcatcgtcat gagccattat acgtggcaca acgtcacgga gtctagccga 900
attactacga agcacgcctt tgccaccctg tctttcctcg ctgagacttt catattttctc 960
tacgtttgga tggatgcgct agacattgag aagtggcggt ccgtttcggg caccctgggc 1020
aaatcgatag ccatactctc catactcatg gggcttgtca tgcttggacg cgcggctttc 1080
gtgttcccgc taagtttctt gtcaaatctg gcgaagaaga atgagcacga aaagatctcc 1140
tggaagcagc aagttgtgat ctggtggagc gggttgatga ggggtgctgt ctctatggcc 1200
ctagcttata acaagtttac cagagccggc catacggagg tgagaggtaa cgaaatcatg 1260
attactagca ccattaccgt cgtgctattc tccacagtgg tgttcgggtc cctgactaaa 1320
ccactgatca ggctccttat gccccaccgc catctgacca tgctctccga cgacagcacc 1380
ccgaagtcac tgactcacc tttgctgaca tccagctcg gaagctccat cgaagagccg 1440
acgcagatac cagccctac aaatattcgt ggcgaattca caactatgac gagaacgggtg 1500
cataggtact ggagaaaatt tgatgacaaa ttcatgcgcc caatgtttgg cggcaggggc 1560
ttcgtaccct tcgtccctgg ttcaccaacg gagaggaatc cccacgatct ttcgaagccc 1620
taa 1623

<210> 12
<211> 540
<212> PRT
<213> Zea mays

<400> 12

Met	Gly	Leu	Gly	Val	Asp	Ala	Glu	Thr	Val	Arg	Leu	Gly	Val	Leu	Ser
1				5					10					15	
Ser	Thr	Ser	Asp	His	Ala	Ser	Val	Val	Ser	Asn	Asn	Phe	Phe	Val	Ala
			20					25					30		
Leu	Leu	Cys	Ala	Cys	Ile	Val	Leu	Gly	His	Leu	Leu	Glu	Glu	Asn	Arg
		35					40					45			
Met	Val	Asn	Glu	Ser	Ile	Thr	Ala	Leu	Leu	Val	Gly	Leu	Gly	Thr	Gly
	50					55					60				
Thr	Val	Ile	Leu	Met	Ile	Ser	Arg	Gly	Val	Ser	Ile	His	Val	Leu	Val
65					70					75					80
Phe	Ser	Glu	Asp	Leu	Phe	Phe	Ile	Tyr	Leu	Leu	Pro	Pro	Ile	Ile	Phe
			85					90						95	
Asn	Ala	Gly	Phe	Gln	Val	Lys	Lys	Lys	Gln	Phe	Phe	Arg	Asn	Phe	Ile
		100						105					110		
Thr	Ile	Ile	Leu	Phe	Gly	Ala	Ile	Gly	Thr	Leu	Ile	Ser	Phe	Val	Ile
		115					120					125			
Ile	Ser	Leu	Gly	Ala	Met	Gly	Leu	Phe	Lys	Lys	Leu	Asp	Val	Gly	Pro
	130					135					140				
Leu	Glu	Leu	Gly	Asp	Tyr	Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ser	Ala	Thr
145					150				155						160
Asp	Ser	Val	Cys	Thr	Leu	Gln	Val	Leu	Asn	Gln	Asp	Glu	Thr	Pro	Leu
			165						170					175	
Leu	Tyr	Ser	Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser
			180					185					190		
Ile	Val	Val	Phe	Asn	Ala	Leu	Gln	Asn	Phe	Asp	Ile	Thr	His	Ile	Asn
		195					200					205			
Ala	Glu	Val	Val	Phe	His	Leu	Leu	Gly	Asn	Phe	Leu	Tyr	Leu	Phe	Leu
	210					215					220				
Leu	Ser	Thr	Val	Leu	Gly	Val	Ala	Thr	Gly	Leu	Ile	Ser	Ala	Leu	Val
225					230					235					240
Ile	Lys	Lys	Ile	Tyr	Phe	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala
			245						250					255	
Leu	Met	Met	Leu	Met	Ala	Tyr	Leu	Ser	Tyr	Met	Leu	Ala	Glu	Leu	Phe
			260					265					270		

<400> 13

```
atgtcaatag gactgacggc cgagaccgtg actaacaagc tagccagcgc cgagcacccc 60
caagtcgtcc ctaattctgt gttcattgcg ctccctctgtc tgtgcctggg gataggccac 120
ctccttgagg agaacagatg ggtcaatgaa tcaataacag ccattctcgt gggcgctgcg 180
actgggaccg tcatcctgct catctcgaaa ggaaaatcga gccacatact tgtgttcgat 240
gaggaattgt ttttcatcta tctactgccg ccaattatit tcaatgccgg gtttcaagta 300
aagaaaaagc aattcttccg caactttata acgattatit tgtttgggtg tattgggact 360
ctgatttctt ttgtaataat ctctcttggg gctatggggg tgttcaagaa acttgatgtt 420
ggtcactcgc agcttgggga ctatcttgca attgggtgcta ttttctcggc aacagattct 480
gtttgcacct tacagggtgt taaccaggat gaaacacccc tactctacag tctgggtatt 540
ggtgaggggg tcgtgaacga cgctacaagt gttgtgctgt ttaatgcagt gcaaaaagatc 600
gacttcgaac accttaccgg agagggtggc ctccagggtt tcggcaactt cctctatctg 660
ttctcaacct caacgggtct gggcatagcc actggggtca ttaccgcctt cgtcctcaag 720
acactctact tcggccgtca tagtactacc cgtgagttgg ccattatggt cctgatggcc 780
tacttgtcct tcatgcttgc tgagttgttc agtctcagtg gtatcattac tgtttttttc 840
tgccggcgtg tcatgtccca tgttacctgg cacaatgtta ctgagtcgtc cagaattacc 900
tctcgccatg tgttcgctat gctaagcttc attgccgaaa cgtttttgtt tctgtacgtg 960
gggacggacg cgcttgactt cacaaagtgg aagacgtctt cgttatcctt tgggaagtcc 1020
ctaggggtat ccagcgtgct cctgggggtg gttctagtcg gtcggggcggc attcgttttc 1080
cccctctcgt tcctgagcaa ccttagtaag aaacaccctg gggaaaaaat cacgatcagg 1140
cagcaggttg taatttggtg ggcaggactt atgagggggc ccgtcagcat cgctttggcg 1200
ttcaacaaat ttacaagggc cggtcacact caggtaagag gaaacgcaat catgatcact 1260
agcaccatca tcgtggtgct tttctctaca gtcgttttcg gcctcctcac caaacgtta 1320
atcaaccttc tcatacccca tcgcaatgca acctccatgt tgtctgacga ctccagccct 1380
aagtctctac acagcccact tttaacctcc caactgataa gctcaatcga ggagcccacg 1440
caaatccgcg ggccgacaaa tatacggggg gagttcatga ccatgacgcg aaccgtgcat 1500
cgctattggc gcaagtttga tgacaagttc atgaggccta tgttcggagg caggggtttt 1560
gtcccgtttg tccaggggtc gcctaccgaa agaagctcac ccgatctatc caaggcatga 1620
```

<210> 14

<211> 539

<212> PRT

<213> Zea mays

<400> 14

```
Met Ser Ile Gly Leu Thr Ala Glu Thr Val Thr Asn Lys Leu Ala Ser
1          5          10          15

Ala Glu His Pro Gln Val Val Pro Asn Ser Val Phe Ile Ala Leu Leu
20          25          30

Cys Leu Cys Leu Val Ile Gly His Leu Leu Glu Glu Asn Arg Trp Val
35          40          45

Asn Glu Ser Ile Thr Ala Ile Leu Val Gly Ala Ala Thr Gly Thr Val
50          55          60

Ile Leu Leu Ile Ser Lys Gly Lys Ser Ser His Ile Leu Val Phe Asp
65          70          75          80

Glu Glu Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala
85          90          95

Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Ile Thr Ile
100         105         110

Ile Leu Phe Gly Ala Ile Gly Thr Leu Ile Ser Phe Val Ile Ile Ser
```

115					120					125					
Leu	Gly	Ala	Met	Gly	Leu	Phe	Lys	Lys	Leu	Asp	Val	Gly	Pro	Leu	Glu
130					135					140					
Leu	Gly	Asp	Tyr	Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ser	Ala	Thr	Asp	Ser
145					150					155					160
Val	Cys	Thr	Leu	Gln	Val	Leu	Asn	Gln	Asp	Glu	Thr	Pro	Leu	Leu	Tyr
				165					170					175	
Ser	Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Val	Val
			180					185					190		
Leu	Phe	Asn	Ala	Val	Gln	Lys	Ile	Asp	Phe	Glu	His	Leu	Thr	Gly	Glu
		195					200					205			
Val	Ala	Leu	Gln	Val	Phe	Gly	Asn	Phe	Leu	Tyr	Leu	Phe	Ser	Thr	Ser
	210					215					220				
Thr	Val	Leu	Gly	Ile	Ala	Thr	Gly	Leu	Ile	Thr	Ala	Phe	Val	Leu	Lys
225					230					235					240
Thr	Leu	Tyr	Phe	Gly	Arg	His	Ser	Thr	Thr	Arg	Glu	Leu	Ala	Ile	Met
			245						250					255	
Val	Leu	Met	Ala	Tyr	Leu	Ser	Phe	Met	Leu	Ala	Glu	Leu	Phe	Ser	Leu
		260						265					270		
Ser	Gly	Ile	Ile	Thr	Val	Phe	Phe	Cys	Gly	Val	Leu	Met	Ser	His	Val
	275						280					285			
Thr	Trp	His	Asn	Val	Thr	Glu	Ser	Ser	Arg	Ile	Thr	Ser	Arg	His	Val
	290					295					300				
Phe	Ala	Met	Leu	Ser	Phe	Ile	Ala	Glu	Thr	Phe	Leu	Phe	Leu	Tyr	Val
305					310					315					320
Gly	Thr	Asp	Ala	Leu	Asp	Phe	Thr	Lys	Trp	Lys	Thr	Ser	Ser	Leu	Ser
				325					330					335	
Phe	Gly	Lys	Ser	Leu	Gly	Val	Ser	Ser	Val	Leu	Leu	Gly	Leu	Val	Leu
			340					345					350		
Val	Gly	Arg	Ala	Ala	Phe	Val	Phe	Pro	Leu	Ser	Phe	Leu	Ser	Asn	Leu
		355					360					365			
Ser	Lys	Lys	His	Pro	Gly	Glu	Lys	Ile	Thr	Ile	Arg	Gln	Gln	Val	Val
	370					375					380				
Ile	Trp	Trp	Ala	Gly	Leu	Met	Arg	Gly	Ala	Val	Ser	Ile	Ala	Leu	Ala
385					390					395					400
Phe	Asn	Lys	Phe	Thr	Arg	Ala	Gly	His	Thr	Gln	Val	Arg	Gly	Asn	Ala
			405						410					415	
Ile	Met	Ile	Thr	Ser	Thr	Ile	Ile	Val	Val	Leu	Phe	Ser	Thr	Val	Val

420

425

430

Phe Gly Leu Leu Thr Lys Pro Leu Ile Asn Leu Leu Ile Pro His Arg
 435 440 445

Asn Ala Thr Ser Met Leu Ser Asp Asp Ser Ser Pro Lys Ser Leu His
 450 455 460

Ser Pro Leu Leu Thr Ser Gln Leu Ile Ser Ser Ile Glu Glu Pro Thr
 465 470 475 480

Gln Ile Pro Arg Pro Thr Asn Ile Arg Gly Glu Phe Met Thr Met Thr
 485 490 495

Arg Thr Val His Arg Tyr Trp Arg Lys Phe Asp Asp Lys Phe Met Arg
 500 505 510

Pro Met Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro
 515 520 525

Thr Glu Arg Ser Ser Pro Asp Leu Ser Lys Ala
 530 535

<210> 15
 <211> 1617
 <212> DNA
 <213> Zea mays

<400> 15
 atggggtatc aggtcgtcgc cgcgcagctg aagctggctt cctcagctga ccacgcaagc 60
 gtggttatca tcacgtctct cgtggccctc ctctgcgctt gcatagtgtt gggccatctt 120
 cttgaagaga atcgtctggct aaacgaatca attacagcat tgataatcgg gctcggaaacg 180
 ggggttgatg ttctattgat cagccgaggt aagaacagcc gcctgcttgt gttctcggag 240
 gacctcttct tcatctatct attgccgccc attattttca atgccgggtt ccaggtgaag 300
 aagaaacagt tcttccggaa ttctatgaca atcacactat tcggtgctgt tggcacaatg 360
 atatccttct tcacaatctc tctcggcgca atagcgacat tcagcagaat gagcattggg 420
 acgctagatg tcgggggattt tctcgtctatt ggagctatct tttctgcaac ggattctgtg 480
 tgcacgctgc aggtcctcca tcaggatgag acgccctttc tgtacagtct ggtattcggg 540
 gagggcgtag tgaacgatgc cacaagtgtt gtactcttca acgcagttca gaagatccag 600
 ttcaccacaca taaatgcatg gacagctctc cagctgatcg gtaactttct ttacctcttc 660
 tccacgagta cactgctcgg tatcgggacc ggcttgatca cagcgtttgt cctgaagaag 720
 ttgtatttcg gcaggcactc cactaccgag gagcttgcca tcatgatctt aatggcctac 780
 ctgtcataca tgcttgccga gttgtttagt ctgtccgggc tcctcacggg ctttttctgt 840
 ggcgtgctaa tgtctcatgt cacatggcat aatgttacgg agtccagcag gacaaccagc 900
 cgtcacgtgt tcgcgacgct ctcgttcata tctgagactt tcatattcct gtatgtgggc 960
 atggacgcac tcgattttcga gaagtggag acctcatcat taagcttcgg tgggaccctg 1020
 ggagttagtg gagtactcat ggggctgggc atgctaggca gagctgcttt tgtctttcct 1080
 ctctcctttc tctccaacct cgccaagaaa caccaaagtg agaaaatttc ttttaggatg 1140
 caggttgatg tttggtgggc ggggtctaat gcgcggcgcg tttccatggc cttggcggtg 1200
 aacaaattca ctcggagcgg ccacaccag ctacatggca atgctatcat gataacttca 1260
 accattaccg tgggtgctgt ctctacgatg gtctttggca tgattacaaa gccactgatc 1320
 aggtgctttt tgcttgcgtc tggacatccg agagaattat cggaaccgtc gtcacccaag 1380
 agcttccata gtctcttct tacctcgcaa cagggatctg acctggagtc gacaaccaat 1440
 atagtcgctc cctctcact tagggggctc ctactaaac caactcacac ggtgcactac 1500
 tactggcgga agttcgatga cgcacttatg agaccggtgt tcgggggacg tggtttcgtg 1560
 ccatttgttc ccggcagccc aaccgagcga aatccaccgg atctgtccaa agcctga 1617

<210> 16
<211> 538
<212> PRT
<213> Zea mays

<400> 16

Met	Gly	Tyr	Gln	Val	Val	Ala	Ala	Gln	Leu	Lys	Leu	Ala	Ser	Ser	Ala
1				5					10					15	
Asp	His	Ala	Ser	Val	Val	Ile	Ile	Thr	Leu	Phe	Val	Ala	Leu	Leu	Cys
			20					25					30		
Ala	Cys	Ile	Val	Leu	Gly	His	Leu	Leu	Glu	Glu	Asn	Arg	Trp	Leu	Asn
		35					40					45			
Glu	Ser	Ile	Thr	Ala	Leu	Ile	Ile	Gly	Leu	Gly	Thr	Gly	Val	Val	Ile
	50					55					60				
Leu	Leu	Ile	Ser	Arg	Gly	Lys	Asn	Ser	Arg	Leu	Leu	Val	Phe	Ser	Glu
65					70				75						80
Asp	Leu	Phe	Phe	Ile	Tyr	Leu	Leu	Pro	Pro	Ile	Ile	Phe	Asn	Ala	Gly
				85					90					95	
Phe	Gln	Val	Lys	Lys	Lys	Gln	Phe	Phe	Arg	Asn	Phe	Met	Thr	Ile	Thr
			100					105					110		
Leu	Phe	Gly	Ala	Val	Gly	Thr	Met	Ile	Ser	Phe	Phe	Thr	Ile	Ser	Leu
		115					120					125			
Gly	Ala	Ile	Ala	Thr	Phe	Ser	Arg	Met	Ser	Ile	Gly	Thr	Leu	Asp	Val
	130						135				140				
Gly	Asp	Phe	Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ser	Ala	Thr	Asp	Ser	Val
145					150					155					160
Cys	Thr	Leu	Gln	Val	Leu	His	Gln	Asp	Glu	Thr	Pro	Phe	Leu	Tyr	Ser
				165					170					175	
Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Val	Val	Leu
			180					185					190		
Phe	Asn	Ala	Val	Gln	Lys	Ile	Gln	Phe	Thr	His	Ile	Asn	Ala	Trp	Thr
		195					200					205			
Ala	Leu	Gln	Leu	Ile	Gly	Asn	Phe	Leu	Tyr	Leu	Phe	Ser	Thr	Ser	Thr
	210					215					220				
Leu	Leu	Gly	Ile	Gly	Thr	Gly	Leu	Ile	Thr	Ala	Phe	Val	Leu	Lys	Lys
225					230					235					240
Leu	Tyr	Phe	Gly	Arg	His	Ser	Thr	Thr	Arg	Glu	Leu	Ala	Ile	Met	Ile
				245					250					255	
Leu	Met	Ala	Tyr	Leu	Ser	Tyr	Met	Leu	Ala	Glu	Leu	Phe	Ser	Leu	Ser
			260					265					270		

Gly Leu Leu Thr Val Phe Phe Cys Gly Val Leu Met Ser His Val Thr
 275 280 285
 Trp His Asn Val Thr Glu Ser Ser Arg Thr Thr Ser Arg His Val Phe
 290 295 300
 Ala Thr Leu Ser Phe Ile Ser Glu Thr Phe Ile Phe Leu Tyr Val Gly
 305 310 315 320
 Met Asp Ala Leu Asp Phe Glu Lys Trp Lys Thr Ser Ser Leu Ser Phe
 325 330 335
 Gly Gly Thr Leu Gly Val Ser Gly Val Leu Met Gly Leu Val Met Leu
 340 345 350
 Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala
 355 360 365
 Lys Lys His Gln Ser Glu Lys Ile Ser Phe Arg Met Gln Val Val Ile
 370 375 380
 Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Leu
 385 390 395 400
 Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His Gly Asn Ala Ile
 405 410 415
 Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Met Val Phe
 420 425 430
 Gly Met Ile Thr Lys Pro Leu Ile Arg Leu Leu Leu Pro Ala Ser Gly
 435 440 445
 His Pro Arg Glu Leu Ser Glu Pro Ser Ser Pro Lys Ser Phe His Ser
 450 455 460
 Pro Leu Leu Thr Ser Gln Gln Gly Ser Asp Leu Glu Ser Thr Thr Asn
 465 470 475 480
 Ile Val Arg Pro Ser Ser Leu Arg Gly Leu Leu Thr Lys Pro Thr His
 485 490 495
 Thr Val His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu Met Arg Pro
 500 505 510
 Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr
 515 520 525
 Glu Arg Asn Pro Pro Asp Leu Ser Lys Ala
 530 535

<210> 17

<211> 2564

<212> DNA

<213> Hordeum vulgare

<400> 17

aacggaacct	tctccagata	ccccgcccgc	gcgaaaagaa	tagaggagaa	tcccgcacctc	60
ccccccccgc	cgggtgcgca	tctgcccccc	ctccttctcc	ctcctcgctc	cccacccccg	120
gtttcccgtg	ccattctttc	cctccccacc	ccggccccgc	gcacgaagca	gcggcggaga	180
cggggccagg	aggaggagga	gctcggctgt	tcttcgtctc	cccgtcgatt	cgtctccgga	240
ttagcgccgc	cggccgttcc	ccgagggctc	cgctccgggtt	gattcgatct	gattgaaaaa	300
gcccgcgtct	ttccccgagg	gcgcgcgctc	gctcgccgga	gctagctgtg	tctcgttcgg	360
ccgggctcaa	ggaagaagag	taacgggcgg	gatggcgctc	gaagtgggtg	cggcgcagtt	420
ggcgcggctg	agcgacgcgc	tggccacctc	ggaccacgcc	tccgtggtct	ccatcaacct	480
cttcgtcgcg	ctgctctgcg	cctgcatcgt	cctcggccac	ctcctcgagg	agaaccgctg	540
gctcaacag	tccatcaccg	ccctcatcat	cgggctgtgc	accggcggtg	tgatcctgat	600
gaccaccaag	gggaagagct	cgcacgtgct	cgtcttcagc	gaggacctct	tcttcatata	660
cctcctccct	cccatcatct	tcaacgccgg	tttccagggtg	aagaagaagc	agttcttccg	720
gaatttcatg	acaatcacat	tattcggcgc	tgtcgggacg	atgatttcat	tcttcacaat	780
ctctcttgct	gccattgcga	tattcagcaa	gatgaacatt	gggacactgg	atgtatcaga	840
ttttctcgca	attggagcca	tcttttccgc	gacagattct	gtctgcactt	tacaggttct	900
caatcaggac	gagacgccct	ttctgtacag	tctagttttc	ggggaagggtg	ttgtgaacga	960
tgccacatca	gtcgtgcttt	tcaacgcgct	ccagaacttc	gatcctaacc	aaatcgatgc	1020
aatcgtcatt	ctgaagttct	tgggaaactt	ctgctactta	ttcgtgtcaa	gcaccttctc	1080
tggagtattt	tctggattgc	tcagtgcata	cataatcaag	aagttataca	taggaaggca	1140
ttctactgac	cgtgagggtg	cgcttatgat	gctcatggcc	tacctctcat	atatgctagc	1200
tgagctgctt	gatttgagtg	gcatcctcac	cgtgttcttc	tgtggtattg	tgatgtcgca	1260
ttatacttgg	cataatgtga	cagagagctc	aagagttaca	acaaagcatg	cttttgcaac	1320
cttgtccttc	attgctgaga	cctttctctt	cctttatgtt	gggatggatg	cactggatat	1380
cgagaagtgg	aaatttgcta	gtgacagccc	tggcaaatcc	atcggaataa	gctcaatttt	1440
gctaggatta	gttctgggtg	gaagagctgc	ttttgtcttc	ccgctttcat	tcttatccaa	1500
cctgacaaag	aagacggagc	tcgaaaaaat	aagctggagg	cagcaaatcg	taatatggtg	1560
ggctgggctg	atgagaggag	ctgtgtcgat	cgctcttgct	tacaataagt	ttacaagatc	1620
tggccacaca	cagctacacg	gcaacgcgat	aatgatcacc	agcaccatca	ctgtcgttct	1680
gtttagcact	atgctgtttg	gcatattgac	aaagcctctg	atccggttcc	tgctgcccgc	1740
gtcgagcaat	ggcgaccctc	cggagccctc	gtcaccgaag	tccctgcact	ctcctctcct	1800
cacaagcatg	ctaggctcgg	acatggaggc	gcctctcccc	atcgtcaggc	cctccagcct	1860
ccggatgctc	atcaccaagc	cgacccacac	catccactac	tactggcgca	agttcgacga	1920
cgcgctgatg	cgtcctatgt	tgcggcggcg	cgggttcgtg	ccctactccc	ctggatcacc	1980
caccgatcca	aacgtaatcg	tggcatgaac	gttgtggaga	gaagagaaaa	gccattacag	2040
cttcaggaga	cactctgaac	tgttgtaact	ggaagagaag	gaggtgctac	agcttcggaa	2100
gaaggcgaag	tctccattac	tattatagtg	tttggtgac	tcggagggcc	gaagaaggcg	2160
cccctctgac	gatggttcag	atgaacggtt	ggttgcggca	ccaacaggaa	gatgaaccct	2220
agtaacggtg	atgcgagtac	catcgcctta	tcggttacga	caagcctgta	cattttttgta	2280
tgtagattaa	caagccaatt	gtaccctatg	agatgagatc	tcctctggca	ggcaggcagg	2340
ccatttcctt	gctccttggc	taggagtctc	tggcctcctg	catatctacc	agtgtctatt	2400
aatctcctcc	cccactttct	agtggattgg	tgtaatggtg	tgtactttac	caagttgtgt	2460
gagatgagtg	atgatcttgt	ggcctgggtg	ctacaaagaa	ctcatctcaa	agttatctat	2520
ctattttcta	tattgaattg	aactgaactt	gtgtcttgaa	ccac		2564

<210> 18

<211> 538

<212> PRT

<213> Hordeum vulgare

<400> 18

Met	Ala	Phe	Glu	Val	Val	Ala	Ala	Gln	Leu	Ala	Arg	Leu	Ser	Asp	Ala
1				5				10						15	

Leu	Ala	Thr	Ser	Asp	His	Ala	Ser	Val	Val	Ser	Ile	Asn	Leu	Phe	Val
			20					25					30		

Ala	Leu	Leu	Cys	Ala	Cys	Ile	Val	Leu	Gly	His	Leu	Leu	Glu	Glu	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35					40					45					
Arg	Trp	Leu	Asn	Glu	Ser	Ile	Thr	Ala	Leu	Ile	Ile	Gly	Leu	Cys	Thr
50						55				60					
Gly	Val	Val	Ile	Leu	Met	Thr	Thr	Lys	Gly	Lys	Ser	Ser	His	Val	Leu
65					70					75					80
Val	Phe	Ser	Glu	Asp	Leu	Phe	Phe	Ile	Tyr	Leu	Leu	Pro	Pro	Ile	Ile
				85					90					95	
Phe	Asn	Ala	Gly	Phe	Gln	Val	Lys	Lys	Lys	Gln	Phe	Phe	Arg	Asn	Phe
			100					105					110		
Met	Thr	Ile	Thr	Leu	Phe	Gly	Ala	Val	Gly	Thr	Met	Ile	Ser	Phe	Phe
		115					120					125			
Thr	Ile	Ser	Leu	Ala	Ala	Ile	Ala	Ile	Phe	Ser	Lys	Met	Asn	Ile	Gly
	130					135					140				
Thr	Leu	Asp	Val	Ser	Asp	Phe	Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ser	Ala
145					150					155					160
Thr	Asp	Ser	Val	Cys	Thr	Leu	Gln	Val	Leu	Asn	Gln	Asp	Glu	Thr	Pro
				165					170					175	
Phe	Leu	Tyr	Ser	Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr
			180					185					190		
Ser	Val	Val	Leu	Phe	Asn	Ala	Leu	Gln	Asn	Phe	Asp	Pro	Asn	Gln	Ile
	195						200					205			
Asp	Ala	Ile	Val	Ile	Leu	Lys	Phe	Leu	Gly	Asn	Phe	Cys	Tyr	Leu	Phe
	210					215					220				
Val	Ser	Ser	Thr	Phe	Leu	Gly	Val	Phe	Ser	Gly	Leu	Leu	Ser	Ala	Tyr
225					230					235					240
Ile	Ile	Lys	Lys	Leu	Tyr	Ile	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val
				245					250					255	
Ala	Leu	Met	Met	Leu	Met	Ala	Tyr	Leu	Ser	Tyr	Met	Leu	Ala	Glu	Leu
			260					265					270		
Leu	Asp	Leu	Ser	Gly	Ile	Leu	Thr	Val	Phe	Phe	Cys	Gly	Ile	Val	Met
	275						280					285			
Ser	His	Tyr	Thr	Trp	His	Asn	Val	Thr	Glu	Ser	Ser	Arg	Val	Thr	Thr
	290					295					300				
Lys	His	Ala	Phe	Ala	Thr	Leu	Ser	Phe	Ile	Ala	Glu	Thr	Phe	Leu	Phe
305					310					315					320
Leu	Tyr	Val	Gly	Met	Asp	Ala	Leu	Asp	Ile	Glu	Lys	Trp	Lys	Phe	Ala
				325					330					335	
Ser	Asp	Ser	Pro	Gly	Lys	Ser	Ile	Gly	Ile	Ser	Ser	Ile	Leu	Leu	Gly

340	345	350
Leu Val Leu Val Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu		
355	360	365
Ser Asn Leu Thr Lys Lys Thr Glu Leu Glu Lys Ile Ser Trp Arg Gln		
370	375	380
Gln Ile Val Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile		
385	390	395
Ala Leu Ala Tyr Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His		
405	410	415
Gly Asn Ala Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser		
420	425	430
Thr Met Leu Phe Gly Ile Leu Thr Lys Pro Leu Ile Arg Phe Leu Leu		
435	440	445
Pro Ala Ser Ser Asn Gly Asp Pro Ser Glu Pro Ser Ser Pro Lys Ser		
450	455	460
Leu His Ser Pro Leu Leu Thr Ser Met Leu Gly Ser Asp Met Glu Ala		
465	470	475
Pro Leu Pro Ile Val Arg Pro Ser Ser Leu Arg Met Leu Ile Thr Lys		
485	490	495
Pro Thr His Thr Ile His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu		
500	505	510
Met Arg Pro Met Phe Gly Gly Arg Gly Phe Val Pro Tyr Ser Pro Gly		
515	520	525
Ser Pro Thr Asp Pro Asn Val Ile Val Ala		
530	535	

<210> 19
 <211> 2422
 <212> DNA
 <213> Triticum aestivum

<400> 19	
atgggggtacc aagtgggtggc ggcgagctg gcgcggctga gcggcgcgct gggcacctcg	60
gaccacgcct ccgtgggtctc catcaccctc ttcgctgcgc tgctctgcgc ctgcatcgctc	120
ctcggccacc tgctcgagga gaaccgctgg ctcaacgagt ccatcaccgc cctcatcatc	180
gggctgtgca ccggcgtggt gatcctgatg accaccaagg ggaagagctc gcacgtgctc	240
gtcttcagcg aggacctctt ctcatcttac ctctgcctc ccatcatctt caacgccggt	300
ttccaggtga agaagaagca gttcttccgg aatttcatgg caatcacact atttggtgcc	360
gttggggacga tgatgtcggt tttcacaata tctcttgctg ccattgcatg attcagcagg	420
atgaacattg ggacactgga tgtatcagat tttcttgcaa ttggagctat cttttccgcg	480
acagattctg tctgcactct acaggttctc aatcaggacg agacgccctt tttgtacagt	540
ctagtgttcg gggaagggtg tgtgaacgat gccacatcgg tcgtgctttt caacgcgctc	600
cagaacttcg atcctaacca gatcgacgcg atcgtcattc ttaagttctt ggggaacttc	660
tgctacttat tcgtgtcaag caccttccct ggagtggtta ctggattgct tagtgcatac	720
gtcatcaaga agttatacat aggaaggcat tctactgacc gtgaggtcgc acttgatgatg	780

ctcatggcct	acctctcata	tatgctagct	gagctgctag	atttgagtgg	tatcctcact	840
gtattcttct	gtgggtattgt	gatgtcacat	tacacctggc	acaacgtgac	agagagctca	900
agagttacaa	caaagcatgc	atttgcaacc	ttgtccttca	tcgctgagac	ttttctcttc	960
ctttatgttg	ggatggatgc	actggatatt	gagaagtgga	aatttgctag	tgacagcccc	1020
ggcaaatacca	ttggaataag	ctcaattttg	ctcgggttg	ttctgggttg	aagagctgct	1080
ttcgtcttcc	cgctctcggt	cttatccaac	ctgacaaaga	agacggagct	cgaaaaaata	1140
agctggaggc	agcaaatcgt	aatatgggtg	gctgggctga	tgagaggagc	tgtgtcgatc	1200
gctcttgctt	acaataagtt	tacaagatct	ggtcacacac	agctgcacgg	caacgcgata	1260
atgatcacca	gcaccatcac	tgctgttctg	tttagcacta	tggtgttttg	cattttgaca	1320
aagcctctga	tccggttcct	actgcccgcg	tcgagcaatg	gcgcgcctc	agatcccgcg	1380
tcaccgaagt	ccctgcactc	tcctctcttc	acaagccagc	taggctcgga	cctggaggcg	1440
cctctcccca	tcgtgaggcc	ctccagcctc	cggatgctca	tcaccaagcc	gaccacacc	1500
atccactact	actggcgcaa	gtttgacgac	gcgctgatgc	gcccgatgtt	cggagggcgc	1560
gggttcgtgc	cctactcccc	aggatcacc	accgatccga	acgtactcgt	ggaatgaacg	1620
tcgcgaagaa	gcaacggaga	agccattaca	gcttcaggag	acactctgaa	ctgtaacagg	1680
aagggaagga	agtgtcacag	cttcagaaga	acgcgaagtc	tccggtaata	ttatagcggt	1740
tggcagactc	ggaaggctga	agaaggcggc	cctccgatga	tggttcagat	gaacgggttg	1800
ttgcggcacc	gacaggaaga	tgaaccctag	taacgggtgat	gcgagtatca	tcatcgctt	1860
atcggttacg	acaaagcctg	tacagttttg	tatgtagatt	aacaagccaa	ttgtatccta	1920
tgagatctcc	gttggcaggc	aggcgtctga	cctcctgcat	ctgcgacgac	cgcggcgtgg	1980
ccaaggccgg	gtgcgggcgg	tcgtacgcgc	cgttcccggc	cgggtgcatg	ttccacagcg	2040
agggcgggct	caagagcttc	gagcacccca	tgaaccgcct	taaggcgctc	cccaggggtg	2100
acagcgaggg	cgatcatgtc	ggcgccaact	tcaaggtcga	cgcttcacc	aagatcaact	2160
ccatgccccg	cgctggcagc	gccaccaact	gggcccgcgc	ctgggacgac	gccgccatct	2220
gatcctcgcc	ggcgccggcg	ttgctctccg	tcgtggcctc	gtcgggcttg	ggcttattgc	2280
attttacttg	tttttctttc	cttggcaatg	tacattctga	tctgatctga	tctgagccgt	2340
gtgtgggcgt	gggcgcgctg	gcacgtacgg	ctgtttgctt	gtacgatgga	ggaataagac	2400
tttgcttcca	gtccaaaaaa	aa				2422

<210> 20

<211> 538

<212> PRT

<213> Triticum aestivum

<400> 20

Met	Gly	Tyr	Gln	Val	Val	Ala	Ala	Gln	Leu	Ala	Arg	Leu	Ser	Gly	Ala
1				5					10					15	

Leu	Gly	Thr	Ser	Asp	His	Ala	Ser	Val	Val	Ser	Ile	Thr	Leu	Phe	Val
			20						25					30	

Ala	Leu	Leu	Cys	Ala	Cys	Ile	Val	Leu	Gly	His	Leu	Leu	Glu	Glu	Asn
			35					40					45		

Arg	Trp	Leu	Asn	Glu	Ser	Ile	Thr	Ala	Leu	Ile	Ile	Gly	Leu	Cys	Thr
			50				55				60				

Gly	Val	Val	Ile	Leu	Met	Thr	Thr	Lys	Gly	Lys	Ser	Ser	His	Val	Leu
65					70					75				80	

Val	Phe	Ser	Glu	Asp	Leu	Phe	Phe	Ile	Tyr	Leu	Leu	Pro	Pro	Ile	Ile
				85					90					95	

Phe	Asn	Ala	Gly	Phe	Gln	Val	Lys	Lys	Lys	Gln	Phe	Phe	Arg	Asn	Phe
			100					105						110	

Met	Ala	Ile	Thr	Leu	Phe	Gly	Ala	Val	Gly	Thr	Met	Met	Ser	Phe	Phe
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115					120					125					
Thr	Ile	Ser	Leu	Ala	Ala	Ile	Ala	Ile	Phe	Ser	Arg	Met	Asn	Ile	Gly
130						135					140				
Thr	Leu	Asp	Val	Ser	Asp	Phe	Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ser	Ala
145					150					155					160
Thr	Asp	Ser	Val	Cys	Thr	Leu	Gln	Val	Leu	Asn	Gln	Asp	Glu	Thr	Pro
				165					170					175	
Phe	Leu	Tyr	Ser	Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr
			180					185					190		
Ser	Val	Val	Leu	Phe	Asn	Ala	Leu	Gln	Asn	Phe	Asp	Pro	Asn	Gln	Ile
			195				200					205			
Asp	Ala	Ile	Val	Ile	Leu	Lys	Phe	Leu	Gly	Asn	Phe	Cys	Tyr	Leu	Phe
	210					215					220				
Val	Ser	Ser	Thr	Phe	Leu	Gly	Val	Phe	Thr	Gly	Leu	Leu	Ser	Ala	Tyr
225						230					235				240
Val	Ile	Lys	Lys	Leu	Tyr	Ile	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val
				245					250					255	
Ala	Leu	Val	Met	Leu	Met	Ala	Tyr	Leu	Ser	Tyr	Met	Leu	Ala	Glu	Leu
			260					265					270		
Leu	Asp	Leu	Ser	Gly	Ile	Leu	Thr	Val	Phe	Phe	Cys	Gly	Ile	Val	Met
			275				280					285			
Ser	His	Tyr	Thr	Trp	His	Asn	Val	Thr	Glu	Ser	Ser	Arg	Val	Thr	Thr
			290			295					300				
Lys	His	Ala	Phe	Ala	Thr	Leu	Ser	Phe	Ile	Ala	Glu	Thr	Phe	Leu	Phe
305						310					315				320
Leu	Tyr	Val	Gly	Met	Asp	Ala	Leu	Asp	Ile	Glu	Lys	Trp	Lys	Phe	Ala
				325					330					335	
Ser	Asp	Ser	Pro	Gly	Lys	Ser	Ile	Gly	Ile	Ser	Ser	Ile	Leu	Leu	Gly
			340					345					350		
Leu	Val	Leu	Val	Gly	Arg	Ala	Ala	Phe	Val	Phe	Pro	Leu	Ser	Phe	Leu
			355				360					365			
Ser	Asn	Leu	Thr	Lys	Lys	Thr	Glu	Leu	Glu	Lys	Ile	Ser	Trp	Arg	Gln
			370			375					380				
Gln	Ile	Val	Ile	Trp	Trp	Ala	Gly	Leu	Met	Arg	Gly	Ala	Val	Ser	Ile
385						390					395				400
Ala	Leu	Ala	Tyr	Asn	Lys	Phe	Thr	Arg	Ser	Gly	His	Thr	Gln	Leu	His
				405					410					415	
Gly	Asn	Ala	Ile	Met	Ile	Thr	Ser	Thr	Ile	Thr	Val	Val	Leu	Phe	Ser

420

425

430

Thr Met Leu Phe Gly Ile Leu Thr Lys Pro Leu Ile Arg Phe Leu Leu
 435 440 445

Pro Ala Ser Ser Asn Gly Ala Ala Ser Asp Pro Ala Ser Pro Lys Ser
 450 455 460

Leu His Ser Pro Leu Leu Thr Ser Gln Leu Gly Ser Asp Leu Glu Ala
 465 470 475 480

Pro Leu Pro Ile Val Arg Pro Ser Ser Leu Arg Met Leu Ile Thr Lys
 485 490 495

Pro Thr His Thr Ile His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu
 500 505 510

Met Arg Pro Met Phe Gly Gly Arg Gly Phe Val Pro Tyr Ser Pro Gly
 515 520 525

Ser Pro Thr Asp Pro Asn Val Leu Val Glu
 530 535

<210> 21

<211> 1726

<212> DNA

<213> Oryza sativa

<400> 21

ggtggccatc	tcgcttgaat	ctgcaggggtg	agctgaggag	gatccactga	ggtggcggcg	60
gtcgaatg	ggctggattt	gggagctctc	gttctcaaat	ccggcgggct	gttgggtctg	120
gactacgact	cgatcgctgc	gatcaacatc	ttcgtggcgc	tgctgtgcag	ctgcattgtg	180
atcgggcacc	tgctggaagg	gaaccgggtg	gtcaatgaat	ccatcaccgc	gcttgtcatg	240
gggctgatca	ctggagggtg	gattctgctc	gtcagtgggtg	ggaagaactc	gcacattctt	300
gtgttcagtg	aggacctctt	cttcatttat	ttgcttcac	cgatcatctt	taatgctggg	360
tttcaagtaa	agaaaaaaca	attcttccgc	aattttatga	caattatatt	atttgggtgct	420
gtggggacat	tgatatcctt	tgtgataatc	tctctagggtg	ccatgacatt	gttcaaaaaa	480
cttgatgttg	gtccactcca	gcttggggac	tatcttgcaa	ttggggctat	cttctcagca	540
acagattctg	tttgacacct	acagggtgctt	aaccaagacg	aaacaccctt	actctatagt	600
ctggtttttg	gtgaaggggt	tgtcaatgat	gctacatctg	ttgtgctctt	taatgcaatt	660
gaagacattg	atattgctaa	ttttgatagc	cttggttctac	tagcgttcat	aggaaatttt	720
ctctacctat	tcttcaccag	tacccttctt	ggagtagttg	ctgggttgct	tagtgccat	780
attattaaga	aactatgttt	tgccagacac	tcaactgaca	gagaagttgc	tatcatgata	840
ctcatggcgt	acctttcata	tatgctgtcg	atgctgctag	atctgagtgg	cattctcact	900
gtgttcttct	ctggaatagt	aatgtcacat	tacacttggc	ataatgtgac	agaaagctct	960
aggattacta	ccaagcacac	ttttgctact	ttatctttca	ttgctgaaat	ttttctatatt	1020
ctctatgttg	ggatggatgc	actggacatt	gaaaaatgga	aattagctag	cagcagtcct	1080
aaaaaaccaa	ttgctttaag	tgcaactata	ttgggcttgg	ttatggttgg	aagagcagca	1140
tttgatttcc	ctttgtcttt	cttatccaat	ctaagtaaaa	aagagacacg	cccaaagatc	1200
tccttcaagc	agcaagtaat	catatgggtg	gcagggtctca	tgagaggagc	agtatcaata	1260
gcacttgctt	atcacaagtt	caccgcatct	ggctacactg	aattgcgaat	caatgctatc	1320
atgatcacca	gcacagtcac	tgttggtctg	ttcagcacaa	tgggttttgg	tttttttacc	1380
aagcctctcc	tcaatctcct	catcccacca	aggcctgaca	tagcagctga	tctctcaagc	1440
cagtcaatca	tagacccact	tcttgggaagc	ctgctgggggt	ctgacttcga	tgtaggccag	1500
ccctcccttc	agaacaacct	tcagcttctt	ctcaccattc	agactcgctc	cgttcatcgc	1560
gtgtggcgca	agtttgatga	tagattcatg	cgcccgatgt	tcggggggccg	aggcttcggt	1620
cctttcgtgc	ctgggttcgcc	agtggagcgg	agcatccatg	gatctcaact	gggcactgtg	1680

actgaggctg aacatagctg agtttgaggt tcagaagggt caagca

1726

<210> 22
<211> 544
<212> PRT
<213> Oryza sativa

<400> 22

Met	Gly	Leu	Asp	Leu	Gly	Ala	Leu	Val	Leu	Lys	Ser	Gly	Gly	Leu	Leu
1			5						10					15	
Val	Ser	Asp	Tyr	Asp	Ser	Ile	Val	Ala	Ile	Asn	Ile	Phe	Val	Ala	Leu
		20						25					30		
Leu	Cys	Ser	Cys	Ile	Val	Ile	Gly	His	Leu	Leu	Glu	Gly	Asn	Arg	Trp
		35					40					45			
Val	Asn	Glu	Ser	Ile	Thr	Ala	Leu	Val	Met	Gly	Leu	Ile	Thr	Gly	Gly
	50					55					60				
Val	Ile	Leu	Leu	Val	Ser	Gly	Gly	Lys	Asn	Ser	His	Ile	Leu	Val	Phe
65					70				75						80
Ser	Glu	Asp	Leu	Phe	Phe	Ile	Tyr	Leu	Leu	Pro	Pro	Ile	Ile	Phe	Asn
			85					90						95	
Ala	Gly	Phe	Gln	Val	Lys	Lys	Lys	Gln	Phe	Phe	Arg	Asn	Phe	Met	Thr
		100						105					110		
Ile	Ile	Leu	Phe	Gly	Ala	Val	Gly	Thr	Leu	Ile	Ser	Phe	Val	Ile	Ile
		115					120					125			
Ser	Leu	Gly	Ala	Met	Thr	Leu	Phe	Lys	Lys	Leu	Asp	Val	Gly	Pro	Leu
	130					135					140				
Gln	Leu	Gly	Asp	Tyr	Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ser	Ala	Thr	Asp
145					150				155						160
Ser	Val	Cys	Thr	Leu	Gln	Val	Leu	Asn	Gln	Asp	Glu	Thr	Pro	Leu	Leu
			165					170						175	
Tyr	Ser	Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Val
		180					185						190		
Val	Leu	Phe	Asn	Ala	Ile	Glu	Asp	Ile	Asp	Ile	Ala	Asn	Phe	Asp	Ser
		195					200					205			
Leu	Val	Leu	Leu	Ala	Phe	Ile	Gly	Asn	Phe	Leu	Tyr	Leu	Phe	Phe	Thr
	210					215					220				
Ser	Thr	Leu	Leu	Gly	Val	Val	Ala	Gly	Leu	Leu	Ser	Ala	Tyr	Ile	Ile
225					230					235					240
Lys	Lys	Leu	Cys	Phe	Ala	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala	Ile
			245						250					255	
Met	Ile	Leu	Met	Ala	Tyr	Leu	Ser	Tyr	Met	Leu	Ser	Met	Leu	Leu	Asp

260						265						270					
Leu	Ser	Gly	Ile	Leu	Thr	Val	Phe	Phe	Ser	Gly	Ile	Val	Met	Ser	His		
		275					280						285				
Tyr	Thr	Trp	His	Asn	Val	Thr	Glu	Ser	Ser	Arg	Ile	Thr	Thr	Lys	His		
	290						295				300						
Thr	Phe	Ala	Thr	Leu	Ser	Phe	Ile	Ala	Glu	Ile	Phe	Leu	Phe	Leu	Tyr		
305					310					315					320		
Val	Gly	Met	Asp	Ala	Leu	Asp	Ile	Glu	Lys	Trp	Lys	Leu	Ala	Ser	Ser		
				325					330					335			
Ser	Pro	Lys	Lys	Pro	Ile	Ala	Leu	Ser	Ala	Thr	Ile	Leu	Gly	Leu	Val		
			340					345					350				
Met	Val	Gly	Arg	Ala	Ala	Phe	Val	Phe	Pro	Leu	Ser	Phe	Leu	Ser	Asn		
		355					360						365				
Leu	Ser	Lys	Lys	Glu	Thr	Arg	Pro	Lys	Ile	Ser	Phe	Lys	Gln	Gln	Val		
	370						375				380						
Ile	Ile	Trp	Trp	Ala	Gly	Leu	Met	Arg	Gly	Ala	Val	Ser	Ile	Ala	Leu		
385					390					395					400		
Ala	Tyr	His	Lys	Phe	Thr	Ala	Ser	Gly	His	Thr	Glu	Leu	Arg	Ile	Asn		
				405					410					415			
Ala	Ile	Met	Ile	Thr	Ser	Thr	Val	Ile	Val	Val	Leu	Phe	Ser	Thr	Met		
			420					425					430				
Val	Phe	Gly	Phe	Phe	Thr	Lys	Pro	Leu	Leu	Asn	Leu	Leu	Ile	Pro	Pro		
		435					440						445				
Arg	Pro	Asp	Ile	Ala	Ala	Asp	Leu	Ser	Ser	Gln	Ser	Ile	Ile	Asp	Pro		
	450						455				460						
Leu	Leu	Gly	Ser	Leu	Leu	Gly	Ser	Asp	Phe	Asp	Val	Gly	Gln	Pro	Ser		
465					470					475					480		
Pro	Gln	Asn	Asn	Leu	Gln	Leu	Leu	Leu	Thr	Ile	Gln	Thr	Arg	Ser	Val		
				485					490					495			
His	Arg	Val	Trp	Arg	Lys	Phe	Asp	Asp	Arg	Phe	Met	Arg	Pro	Met	Phe		
			500					505					510				
Gly	Gly	Arg	Gly	Phe	Val	Pro	Phe	Val	Pro	Gly	Ser	Pro	Val	Glu	Arg		
		515					520						525				
Ser	Ile	His	Gly	Ser	Gln	Leu	Gly	Thr	Val	Thr	Glu	Ala	Glu	His	Ser		
	530						535				540						

<210> 23

<211> 1902

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 23

```
atgctatcca aggtattgct gaatatagct ttcaagggtgc tgttaaccac cgccaagaga      60
gcagttgatc ctgacgatga tgatgaactt ctaccttccc cggatctccc gggtagcgat      120
gaccctattg caggtgatcc tgatgtagac ttaaaccctg ttacagaaga aatgttctct      180
tcatgggcat tgttcattat gttgctccta ttgatctctg cattgtggtc tagttactat      240
ttaactcaga aacgaattag ggcagtgcat gaaactgtgc tttctatfff ttatggtatg      300
gttattggct tgataataag gatgtccccc gggcattata ttcaagatac ggttactfff      360
aattcatcct acttttttaa tgttctattg ccgccaatta ttttaaatag tgggtacgag      420
ttgaatcaag tgaacttttt caataatatg ttatctatct taattttcgc cataccgggc      480
accttcatat ctgctgtggg tattggaatc atattgtata tctggacctt tttaggacta      540
gagagtattg acatttcatt cgcagatgca atgtctgttg gtgctacatt atctgtacc      600
gaccctgtta caattctttc aattttcaat gcgtataaag tggatcctaa gctatatacc      660
atcatttttg gagaatcact gttaaataat gccatctcta ttgttatgtt tgaaacctgt      720
caaaaatttc atggtcaacc tgcaacattt tcgtcggttt ttgaaggggc aggcctcttt      780
ttgatgactt tctccgtttc gttgttgata ggcgttctta taggaattct tgttgctctt      840
ctgttgaaac aactcacat aaggcgctat cctcaaattg agagttgttt gatcttgttg      900
attgcttatg aatcctatft tttctccaac ggttgccata tgtccggtat cgtctccttg      960
ttattttgcg gaattactft aaaacattac gcctattata acatgtcaag aagatcacag     1020
atcaccatta agtatattft ccaactattg gcaagattat cagagaattt catctttatc     1080
tatctagggt tagaactftt tactgaagta gaactagtct ataagccact gctaattatt     1140
gtggcagcta tttctatatg tgttgctcgt tgggtgtgctg tgttcccatt gtcgcaattt     1200
gttaactgga tatatagagt aaagacaatc agatctatga gcggcataac cggagaaaat     1260
atftctgttc ccgatgaaat accctacaat taccaaatga tgacattttg ggcaggttta     1320
cgtgggtgctg ttgggtgtcgc cttggcggtg ggaattcaag gtgagtataa gttcactfta     1380
ttggcaacgg tccttgttgt tgttgfttta acagttatca tttttggggg cactactgca     1440
ggaatgtag aagftttaaa tattaagact ggttgcataa gtgaagaaga tacatctgat     1500
gacgagtttg atatagaggc tccaagggcg ataaaattat tgaacggtag ttctattcag     1560
acagatttgg gcccatattc tgacaacaat tctccagata tttcaattga ccaattcgcg     1620
gtcagcagta acaagaatct cccaataaac atatccacaa ctggtggtaa tacttttgga     1680
ggccttaatg aaaactgagaa tactagccct aacccgcaa ggtcttctat ggataagcgt     1740
aatttgagag ataaaactggg aacaatctft aattccgact cacaatggtt tcaaaattft     1800
gatgaacagg tattgaagcc agtattcttg gacaacgttt ctccatcctt acaagattcg     1860
gctacgcaat cacctgcaga tttctcttcc caaaaccact ag                               1902
```

<210> 24

<211> 633

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 24

```
Met Leu Ser Lys Val Leu Leu Asn Ile Ala Phe Lys Val Leu Leu Thr
1                               10                   15

Thr Ala Lys Arg Ala Val Asp Pro Asp Asp Asp Asp Glu Leu Leu Pro
20                               25                   30

Ser Pro Asp Leu Pro Gly Ser Asp Asp Pro Ile Ala Gly Asp Pro Asp
35                               40                   45

Val Asp Leu Asn Pro Val Thr Glu Glu Met Phe Ser Ser Trp Ala Leu
50                               55                   60

Phe Ile Met Leu Leu Leu Leu Ile Ser Ala Leu Trp Ser Ser Tyr Tyr
65                               70                   75                   80

Leu Thr Gln Lys Arg Ile Arg Ala Val His Glu Thr Val Leu Ser Ile
```

85

90

95

Phe Tyr Gly Met Val Ile Gly Leu Ile Ile Arg Met Ser Pro Gly His
 100 105 110

Tyr Ile Gln Asp Thr Val Thr Phe Asn Ser Ser Tyr Phe Phe Asn Val
 115 120 125

Leu Leu Pro Pro Ile Ile Leu Asn Ser Gly Tyr Glu Leu Asn Gln Val
 130 135 140

Asn Phe Phe Asn Asn Met Leu Ser Ile Leu Ile Phe Ala Ile Pro Gly
 145 150 155 160

Thr Phe Ile Ser Ala Val Val Ile Gly Ile Ile Leu Tyr Ile Trp Thr
 165 170 175

Phe Leu Gly Leu Glu Ser Ile Asp Ile Ser Phe Ala Asp Ala Met Ser
 180 185 190

Val Gly Ala Thr Leu Ser Ala Thr Asp Pro Val Thr Ile Leu Ser Ile
 195 200 205

Phe Asn Ala Tyr Lys Val Asp Pro Lys Leu Tyr Thr Ile Ile Phe Gly
 210 215 220

Glu Ser Leu Leu Asn Asp Ala Ile Ser Ile Val Met Phe Glu Thr Cys
 225 230 235 240

Gln Lys Phe His Gly Gln Pro Ala Thr Phe Ser Ser Val Phe Glu Gly
 245 250 255

Ala Gly Leu Phe Leu Met Thr Phe Ser Val Ser Leu Leu Ile Gly Val
 260 265 270

Leu Ile Gly Ile Leu Val Ala Leu Leu Leu Lys His Thr His Ile Arg
 275 280 285

Arg Tyr Pro Gln Ile Glu Ser Cys Leu Ile Leu Leu Ile Ala Tyr Glu
 290 295 300

Ser Tyr Phe Phe Ser Asn Gly Cys His Met Ser Gly Ile Val Ser Leu
 305 310 315 320

Leu Phe Cys Gly Ile Thr Leu Lys His Tyr Ala Tyr Tyr Asn Met Ser
 325 330 335

Arg Arg Ser Gln Ile Thr Ile Lys Tyr Ile Phe Gln Leu Leu Ala Arg
 340 345 350

Leu Ser Glu Asn Phe Ile Phe Ile Tyr Leu Gly Leu Glu Leu Phe Thr
 355 360 365

Glu Val Glu Leu Val Tyr Lys Pro Leu Leu Ile Ile Val Ala Ala Ile
 370 375 380

Ser Ile Cys Val Ala Arg Trp Cys Ala Val Phe Pro Leu Ser Gln Phe

385		390		395		400
Val Asn Trp Ile Tyr Arg Val Lys Thr Ile Arg Ser Met Ser Gly Ile						
	405			410		415
Thr Gly Glu Asn Ile Ser Val Pro Asp Glu Ile Pro Tyr Asn Tyr Gln						
	420		425		430	
Met Met Thr Phe Trp Ala Gly Leu Arg Gly Ala Val Gly Val Ala Leu						
	435		440		445	
Ala Leu Gly Ile Gln Gly Glu Tyr Lys Phe Thr Leu Leu Ala Thr Val						
	450		455		460	
Leu Val Val Val Val Leu Thr Val Ile Ile Phe Gly Gly Thr Thr Ala						
	465		470		475	480
Gly Met Leu Glu Val Leu Asn Ile Lys Thr Gly Cys Ile Ser Glu Glu						
	485		490			495
Asp Thr Ser Asp Asp Glu Phe Asp Ile Glu Ala Pro Arg Ala Ile Asn						
	500		505			510
Leu Leu Asn Gly Ser Ser Ile Gln Thr Asp Leu Gly Pro Tyr Ser Asp						
	515		520		525	
Asn Asn Ser Pro Asp Ile Ser Ile Asp Gln Phe Ala Val Ser Ser Asn						
	530		535		540	
Lys Asn Leu Pro Asn Asn Ile Ser Thr Thr Gly Gly Asn Thr Phe Gly						
	545		550		555	560
Gly Leu Asn Glu Thr Glu Asn Thr Ser Pro Asn Pro Ala Arg Ser Ser						
	565		570			575
Met Asp Lys Arg Asn Leu Arg Asp Lys Leu Gly Thr Ile Phe Asn Ser						
	580		585			590
Asp Ser Gln Trp Phe Gln Asn Phe Asp Glu Gln Val Leu Lys Pro Val						
	595		600			605
Phe Leu Asp Asn Val Ser Pro Ser Leu Gln Asp Ser Ala Thr Gln Ser						
	610		615		620	
Pro Ala Asp Phe Ser Ser Gln Asn His						
	625		630			

<210> 25

<211> 1857

<212> DNA

<213> Magnaporthe grisea

<400> 25

atgacttttcg atatcgccgg caacctcctg gagctcacca ggcgcgctgc cgaggaaccc	60
gaacctggag gaatggcagt tggccttgcc ctgcgagtgt ttgccgtcga tggactccag	120
gacctcgtca gcttcgatta ccaaattctt ttcaacctcc tccttccacc catcatcctc	180
tcgtccgggt acgagttaca tcaggccaac ttcttccggc acatcggaac aattctcacg	240

ttcgcatttg	ctggcacgtt	cctgtctgca	gtagtcatcg	gtgttatact	atggcctttac	300
actcgcgtac	ccctcgaggg	gctcaccatg	aactggatcg	atgccatatac	tgttggcgca	360
actttgtcag	ctaccgatcc	tgtcaccatc	atagccatct	tcaactcgta	caaggtggac	420
ccgaagctgt	ataccatcat	ctttggagag	gccatcctca	atgacgctgt	ggccattgtc	480
atcttcgagt	cggcgcaaaa	gtccgccagg	ggcttgacca	aaggcagcgc	tgctggcatc	540
tctaccttct	tctggggttt	ctggattttc	ttgagggaact	tcttcggcag	cttgttcatc	600
ggggcgcttc	ttggcatcct	caccgcgctc	atgctcaagt	acacgtacct	caggagggtt	660
cccaagctgg	agagctgctt	gattgtgctt	attgcttacg	ccacgtacta	cttttcccag	720
gccatacaca	tgtctggaat	tgtgtcactg	ttgttctgcg	gaatcacact	caaacactat	780
gcatacttca	acatgtcgcg	aagaactcag	cttacgacca	agtacatgtt	ccaggtcctc	840
gcacaactgt	ctgagaactt	tatctttatt	tacctgggtg	tttccctctt	tacggacaag	900
gatctccagt	tccagcccct	cctcatcatt	gtcactgtca	tggcgggtgtg	cgcagctcgc	960
tgggttgccg	tattcccact	ctcgtgggcc	atcaactggg	tccacaagta	ccgggcagaa	1020
agacgtggca	tcaagaacgt	gcccaggagg	ctgccgtaca	agtaccaagg	catgctgttc	1080
tgggcagggg	tgcgtggagc	ggtcgggtgtt	gccctggccg	cgttggttgac	ggccaaggac	1140
caccgtgcat	tcaaggcgac	cgttctgggt	gtgggtgtgc	tcaactgtcat	catatttggt	1200
ggcactacgg	tcaacgtgct	tgaaatcctc	gagatccgca	cgggagtgac	ggatgagatc	1260
gattctgacg	atgaattcga	catcgaggca	gttgggggct	actacaagcg	atcgggtaac	1320
ggaataggtt	atagcccggc	cgggcgcaat	ggtgttggtc	ccctggacac	acgtccaggt	1380
cggagacgtg	acagtaatgg	cgccgtcggg	ggaagagacg	cgagcggctg	gagctcagga	1440
catagatctc	ccttgagtgc	ggcaaggcct	ggcagtctcg	tccgtacagg	gtcaacacgc	1500
gaagaagcgg	aaagactgga	cctccttggc	aaccgcggcg	gctcgacaga	ctcggatgac	1560
tttgggagcg	acattgacac	gtcggacctg	ccgccaccag	cccctaggag	acgatccagc	1620
ccaatgccgc	ctacggggcg	cgaagaggca	gctggtttgc	cagcgggggg	gagcaggaca	1680
aggtcgaaca	cagagacggg	tggcttgctg	gccacggccg	cgatccgccca	gctgttcagc	1740
accgaggacc	caacagccct	gttcaggcag	ctggacgagg	actacatcaa	accgaagcta	1800
ctgctcgatg	gcggtgccgg	ccgtgggaac	ggtggtggcg	ctggcggatc	gagttag	1857

<210> 26

<211> 618

<212> PRT

<213> Magnaporthe grisea

<400> 26

Met	Thr	Phe	Asp	Ile	Ala	Gly	Asn	Leu	Leu	Glu	Leu	Thr	Arg	Arg	Ala
1				5				10						15	

Ala	Glu	Glu	Pro	Glu	Pro	Gly	Gly	Met	Ala	Val	Gly	Leu	Ala	Leu	Arg
	20							25				30			

Val	Phe	Ala	Val	Asp	Gly	Leu	Gln	Asp	Leu	Val	Ser	Phe	Asp	Tyr	Gln
	35					40					45				

Ile	Phe	Phe	Asn	Leu	Leu	Leu	Pro	Pro	Ile	Ile	Leu	Ser	Ser	Gly	Tyr
	50					55					60				

Glu	Leu	His	Gln	Ala	Asn	Phe	Phe	Arg	His	Ile	Gly	Thr	Ile	Leu	Thr
65				70						75				80	

Phe	Ala	Phe	Ala	Gly	Thr	Phe	Leu	Ser	Ala	Val	Val	Ile	Gly	Val	Ile
				85					90					95	

Leu	Trp	Leu	Tyr	Thr	Arg	Val	Pro	Leu	Glu	Gly	Leu	Thr	Met	Asn	Trp
		100						105						110	

Ile	Asp	Ala	Ile	Ser	Val	Gly	Ala	Thr	Leu	Ser	Ala	Thr	Asp	Pro	Val
		115						120							

Thr	Ile	Ile	Ala	Ile	Phe	Asn	Ser	Tyr	Lys	Val	Asp	Pro	Lys	Leu	Tyr	130	135	140	
Thr	Ile	Ile	Phe	Gly	Glu	Ala	Ile	Leu	Asn	Asp	Ala	Val	Ala	Ile	Val	145	150	155	160
Ile	Phe	Glu	Ser	Ala	Gln	Lys	Ser	Ala	Arg	Gly	Leu	Thr	Lys	Gly	Ser	165	170	175	
Ala	Ala	Gly	Ile	Ser	Thr	Phe	Phe	Trp	Gly	Phe	Trp	Ile	Phe	Leu	Arg	180	185	190	
Asp	Phe	Phe	Gly	Ser	Leu	Phe	Ile	Gly	Ala	Leu	Leu	Gly	Ile	Leu	Thr	195	200	205	
Ala	Leu	Met	Leu	Lys	Tyr	Thr	Tyr	Leu	Arg	Arg	Phe	Pro	Lys	Leu	Glu	210	215	220	
Ser	Cys	Leu	Ile	Val	Leu	Ile	Ala	Tyr	Ala	Thr	Tyr	Tyr	Phe	Ser	Gln	225	230	235	240
Ala	Ile	His	Met	Ser	Gly	Ile	Val	Ser	Leu	Leu	Phe	Cys	Gly	Ile	Thr	245	250	255	
Leu	Lys	His	Tyr	Ala	Tyr	Phe	Asn	Met	Ser	Arg	Arg	Thr	Gln	Leu	Thr	260	265	270	
Thr	Lys	Tyr	Met	Phe	Gln	Val	Leu	Ala	Gln	Leu	Ser	Glu	Asn	Phe	Ile	275	280	285	
Phe	Ile	Tyr	Leu	Gly	Val	Ser	Leu	Phe	Thr	Asp	Lys	Asp	Leu	Gln	Phe	290	295	300	
Gln	Pro	Leu	Leu	Ile	Ile	Val	Thr	Val	Met	Ala	Val	Cys	Ala	Ala	Arg	305	310	315	320
Trp	Val	Ala	Val	Phe	Pro	Leu	Ser	Trp	Ala	Ile	Asn	Trp	Phe	His	Lys	325	330	335	
Tyr	Arg	Ala	Glu	Arg	Arg	Gly	Ile	Lys	Asn	Val	Pro	Glu	Glu	Leu	Pro	340	345	350	
Tyr	Lys	Tyr	Gln	Gly	Met	Leu	Phe	Trp	Ala	Gly	Leu	Arg	Gly	Ala	Val	355	360	365	
Gly	Val	Ala	Leu	Ala	Ala	Leu	Leu	Thr	Ala	Lys	Asp	His	Arg	Ala	Phe	370	375	380	
Lys	Ala	Thr	Val	Leu	Val	Val	Val	Val	Leu	Thr	Val	Ile	Ile	Phe	Gly	385	390	395	400
Gly	Thr	Thr	Val	Asn	Val	Leu	Glu	Ile	Leu	Glu	Ile	Arg	Thr	Gly	Val	405	410	415	
Thr	Asp	Glu	Ile	Asp	Ser	Asp	Asp	Glu	Phe	Asp	Ile	Glu	Ala	Val	Gly	420	425	430	

Gly Tyr Tyr Lys Arg Ser Gly Asn Gly Ile Gly Tyr Ser Pro Ala Gly
 435 440 445
 Arg Asn Gly Val Val Pro Leu Asp Thr Arg Pro Gly Arg Arg Arg Asp
 450 455 460
 Ser Asn Gly Ala Val Gly Gly Arg Asp Ala Ser Gly Trp Ser Ser Gly
 465 470 475 480
 His Arg Ser Pro Leu Ser Ala Ala Arg Pro Gly Ser Leu Val Arg Thr
 485 490 495
 Gly Ser Thr Arg Glu Glu Ala Glu Arg Leu Asp Leu Leu Gly Asn Pro
 500 505 510
 Gly Gly Ser Thr Asp Ser Asp Asp Phe Gly Ser Asp Ile Asp Thr Ser
 515 520 525
 Asp Leu Pro Pro Pro Ala Pro Arg Arg Arg Ser Ser Pro Met Pro Pro
 530 535 540
 Thr Gly Asp Glu Glu Ala Ala Gly Leu Pro Ala Gly Gly Ser Arg Thr
 545 550 555 560
 Arg Ser Asn Thr Glu Thr Gly Gly Leu Ser Ala Thr Ala Ala Ile Arg
 565 570 575
 Gln Leu Phe Ser Thr Glu Asp Pro Thr Ala Leu Phe Arg Gln Leu Asp
 580 585 590
 Glu Asp Tyr Ile Lys Pro Lys Leu Leu Leu Asp Gly Gly Ala Gly Arg
 595 600 605
 Gly Asn Gly Gly Gly Ala Gly Gly Ser Ser
 610 615

<210> 27
 <211> 654
 <212> DNA
 <213> *Oryza sativa*

<400> 27
 cttctacatc ggcttaggtg tagcaacacg actttattat tattattatt attattatta 60
 ttattttaca aaaatataaa atagatcagt ccctcaccac aagtagagca agttggtgag 120
 ttattgtaaa gttctacaaa gctaatttaa aagttattgc attaacttat ttcattattac 180
 aaacaagagt gtcaatggaa caatgaaaac catatgacat actataattt tgtttttatt 240
 attgaaatta tataattcaa agagaataaa tccacatagc cgtaaagttc tacatgtggt 300
 gcattaccaa aatatatata gcttacaaaa catgacaagc ttagtttgaa aaattgcaat 360
 ccttatcaca ttgacacata aagtgagtga tgagtcataa tattattttc tttgctaccc 420
 atcatgtata tatgatagcc acaaagttac tttgatgatg atatcaaaga acatttttag 480
 gtgcacctaa cagaatatcc aaataatatg actcacttag atcataatag agcatcaagt 540
 aaaactaaca ctctaaagca accgatggga aagcatctat aaatagacaa gcacaatgaa 600
 aatcctcatc atccttcacc acaattcaaa tattatagtt gaagcatagt agta 654

<210> 28

<211> 941
<212> DNA
<213> *Oryza sativa*

<400> 28
gataatgagc attgcatgtc taagttataa aaaattacca catatTTTTT ttgtcacact 60
tgTTTgaagt gcagTTTatc tatcTTTata catatattta aactTTTactc tacgaataat 120
ataatctata gtactacaat aatatcagtg tTTtagagaa tcatataaat gaacagttag 180
acatggTcta aaggacaatt gagtattttg acaacaggac tctacagttt tatcTTTtta 240
gtgtgcatgt gTTctcTTTt tTTTtgcaa atagcttcac ctatataata cttcatccat 300
tttattagta catccattta gggTTtaggg ttaatggTTt ttatagacta atTTTTTtag 360
tacatctatt ttattctatt ttagcctcta aattaagaaa actaaaactc tattTTtagtt 420
TTTTtattta ataatttaga tataaaatag aataaaataa agtgactaaa aattaaacaa 480
atacccttta agaaattaaa aaaactaagg aaacattTTTt cttgTTTcga gtagataatg 540
ccagcctgtt aaacgccgtc gacgagtcta acggacacca accagcgaac cagcagcgtc 600
gcgtcgggcc aagcgaagca gacggcacgg catctctgtc gctgcctctg gacccctctc 660
gagagtTccg ctccaccgtt ggacttgtc cgctgtcggc atccagaaat tgcgtggcgg 720
agcggcagac gtgagccggc acggcaggcg gcctcctcct cctctcacgg cacggcagct 780
acgggggatt cTTTcccac cgctccttcg cTTTcccttc ctcgcccgc gtaataaata 840
gacacccct ccacaccctc tttccccaac ctcgtgttgt tcggagcgca cacacacaca 900
accgatctc ccccaaatcc acccgtcggc acctccgctt c 941

<210> 29
<211> 50
<212> DNA
<213> Artificial sequence

<220>
<223> primer: prm3122

<400> 29
ggggacaagt ttgtacaaaa aagcaggctt cacaatgggg atggaggtgg 50

<210> 30
<211> 48
<212> DNA
<213> Artificial sequence

<220>
<223> primer: prm3123

<400> 30
ggggaccact ttgtacaaga aagctgggtg cactgttcat cttcctcc 48